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OM protein -
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_36:*
1: /SIDS1/gcgda
2: /SIDS1/gcgda
3: /SIDS1/gcgda
4: /SIDS1/gcgda
5: /SIDS1/gcgda
6: /SIDS1/gcgda
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-316-163-11
1876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       November 21, 2000, 16:43:45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             268485 seqs, 34193795 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                            /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1988.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA1989.DAT:*
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225.356 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	345.5	10 347.5 18.5										Result Query No. Score Match
		.5 543										y h Length DB
Ľ	13	13	10	20	19	19	13	12	20	18	18	!
0328C8	R28547	R28557	P92219	Y55751	W45899	W73147	R28570	R13490	Y55752	W39155	W39154	ID
CR1-4 (114S) analo	CR1-4 (52S, 53S, 5	CR1-4 (99H, 103E)	CR1 protein. Homo	Human C3b/C4b rece	Human complement r	Amino acid sequenc	CR1-4 (266-274 KLK	Human C4 binding p	Human CR1 protein	Clone prrs9fH410 C	Human partial Comp	Description

Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor

N-PSDB; V02790.

45	44	43	42	41	40	39	38	37	36	35	34	ω u	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
317	w	327.5	329	w	$\frac{3}{2}$	32	ω	333.5	34	35	$\frac{\omega}{5}$	ω S	336	336.5	6	σ	æ	8	8	9	339.5	9	9	0	0	$\mathbf{-}$	\vdash	\vdash	\mathbf{r}	μ.	-	ь.
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577	450	450	453	646	543	543	543	543	543	543	543	543	1537	2039	543	543	543	543	543	543	543	543	543	543	543	2039	543	543	543	543	543	543
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389	Y55754	575	575	575	855	854	854	854	855	856	856	855	86	σ	56	55	56	55	54	56		5	55	54	54	81	57	56	56	56	55	5
Membrane co-factor	Human CR1 protein			Human CR1 protein	4 - 1	-4 (35E,	-4 (44T, 47D,	-4 (35E)	-4 (92T, 94H)	-4 (318R,	-4 (115T)	-4 (78T, 7	tial hum	OMC	-4 (116K	-4 (94H)	-4 (116K	-4 (65T)	-4 (64K,	-4 (318-3	-4 (117P	-4 (109N,	_	-4 (57V,	-4 (37Y) a	ю	ù	CR1-4 (369-376 STK	-4 (347T,	-4 (121Q) a	-4 (85R,	-4 (64K) anal

ALIGNMENTS

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RESULT
W39154
ID W3
06-MAR-1997;
09-APR-1996;
09-APR-1996;
06-MAR-1997;
                                                                                                                                                                                                                                                                       W39154 standard; Protein; 240
                               WPI; 1997-512742/47.
                                                Enfield DL,
                                                                                                                                                                                             urogenital cancer; medicament; modulator.
                                                                                                                                                                                                      Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                      Human partial Complement factor H protein fragment 1.
                                                                                                                                                                                                                                      27-APR-1998 (first entry)
                                                                                                                                                                                                                                                        W39154;
                                                                 (BARD-) BARD DIAGNOSTIC SCI INC
                                                                                                                            09-APR-1997;
                                                                                                                                            16-OCT-1997.
                                                                                                                                                            WO9738136-A1.
                                                                                                                                                                            Homo sapiens
                                                Hass GM,
                                                                                 97US-0812481.
96US-0015083.
96US-0630048.
97US-0038614.
                                                                                                                            97WO-US05710
                                                  Kinders RJ;
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                                                                                                                                                                    06-MAR-1997;
09-APR-1996;
09-APR-1996;
06-MAR-1997;
Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                          Complement factor H; tumour associated antigen; renal cancer; urogenital cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This partial protein sequence represents a region of the human tumour associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens isolated from clone prBB9FH410 (see W39155). The detection of such proteins and a CFH antigens can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                         (BARD-) BARD DIAGNOSTIC SCI INC.
                                                                                                                                                                                                                                           09-APR-1997;
                                                                                                                                                                                                                                                                      16-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                               Clone pRRB9FH410 CFH related protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               W39155;
                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W39155 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78 FILTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  related antigen, or nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ,
                                                                              1997-512742/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHGGL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dysplrikhrtgdeityqcrngfypatrgntakctstgwipaprctlkpcdypdikhggl 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ftltggnvfeygvkavytcnegyqllgeinyrecdtdgwtndipicevvkclpvtapeng 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                            DL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 AA;
                                                                                                            Hass GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                   97US-0812481.
96US-0015083.
96US-0630048.
97US-0038614.
                                                                                                                                                                                                                                          97WO-US05710.
                                                                                                                                                                                                                                                                                                                                                       medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72.6%; Score 1362; DB LU;
100.0%; Pred. NO. 9.5e-96;
^. Mismatches 0;
                                                                                                            Kinders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
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RESULT
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Best Local
                                                                                                                                                         03-APR-1989;
06-DEC-1974;
24-FEB-1993;
             WPI; 1999-633357/54
                                         Marsh HC,
                                                     Concino MF,
                                                                                                                                                                                                                                                                                                                                            C3B/C4B receptor; CRI protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; long homologous repeat; LHR; SCR;
                                                                                 (UYJO ) UNIV JOHNS HOPKINS.
(BGHM ) BRIGHAM & WOMENS HOSPITAL.
(AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
                                                                                                                                             01-APR-1988;
                                                                                                                                                                                                                   06-JUN-1995;
                                                                                                                                                                                                                                               09-NOV-1999
                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                   short consensus repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Y55752 standard; Protein; 496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CPH). The detection of this protein and a CPH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                      Human CR1 protein LHR-A SCR fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYP 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER
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                                      Carson GR;
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                                                     Wong WW,
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                                                                                                                                             88US-0176532
                                                                                                                                                         74US-0350238.
93US-0026134.
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99.5%;
                                                     Makrides SC,
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                                                    Klickstein LB,
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                                                    Fearon
                                                  DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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  FTT FH XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A human C3B/C4B receptor (CR1) protein having antiinflammatory and cardiant activity - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 10; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a human C3B/C4B receptor (CR1) protein. The CR1
                                                                                                                                                                                                                                                                                    30-OCT-1991 (first entry)
                                                                                                                                                                                                                                                                                                                               R13490;
                                                                                                                                                                                                                                                                                                                                                                      R13490 standard; Protein; 581 AA
                                                                                                                                                                                                                                      Human C4 binding protein.
                                                                                                                                                                           short consensus repeat.
                    Protein
                                                               Peptide
                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 325 gqevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115 GWTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVREVCNSG-----YKIE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              104 --rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtv 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          269 GDEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 gfvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              222 GYEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN-------GDYSPLRIKHRT 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
                                                                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          iwdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelv 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiicclknsvwtgakd 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGE-WVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gepsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqp 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GDEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNM 221
                                                                                                                                                                                             monomer; complement protein; pJOD.C4bp.3; SCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         496 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
/label= signal_peptide
33..581
/label= C4bp
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.8%; Score 353; DB 20; 29.8%; Pred. No. 3.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54; Mismatches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 496;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

Qy Qy Db

78

103 -- lrngqveiktdlsfgsqiefscsegffligsttsr-cevqdrgvgwshplpqceivkc 159

FTLTGGNV-----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC 128

Matches

100;

Conservative

50;

Mismatches

Indels

50;

Gaps

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SOXCOCCCCCCCX PX PTTXX PXXX PXXX PXXX PXXX PTTXX PXXX PTTXX PXXX PTTXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXXX PXX PXX PXXX PXXX PXXX PXXX PXXX PXX PXXX PXX PXXX PXXX PXXX PXXX P
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Best Local Similarity
                                                                                                                                                              cysteine residue bonds with the fourth. This secondary structure is responsible for the conformational flexibility of the C4bp monomer. The invention covers fusion proteins in which the monomer sequence, or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) is fused to the C-terminal of a protein such as a viral receptor, cell ligand, a bacterial, viral or parasitic immunogen, enzyme, cytokine, toxin, etc. See also 013243-51.
                                                                                                                                                                                                                                                                                                                                                   This sequence was deduced from human hepatocyte (Hep G2) cDNA obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCI the first cysteine residue bonds with the third and the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional moiety, e.g. AZT, useful as delivery vehicles in diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; Q13242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pasek MP, Winkler G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09111461-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Regior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Regior
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Regior
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Fig 1; 105pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-252613/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BIOG-) BIOGEN INC
                                                                                                          581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0470888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91WO-US00567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "intradomain"
65..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "responsible for multimer assembly" 34..80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33..93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           346..406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156..219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label= SCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     abel=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..345
  18.8%; 29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Liu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCR3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SCR5
  Score 353; DB 12;
Pred. No. 4.4e-19;
                            Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are disclosed in which certain
                                                                                                                                        Complement activity regulator protein analogues - useful for treating auto: immune diseases, to suppress transplant rejection,
                                                                                                Example 8; Page 18 and R11810; 23pp; English.
                                                                                                                                                                                       WPI; 1992-375009/46
                                                                                                                                                                                                                   Atkinson JP,
                                                                                                                                                                                                                                                                         03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference
                                                                                                                                for diagnosis etc.
                                                                                                                                                                                                                                           (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                   28-APR-1992;
                                                                                                                                                                                                                                                                                                                                11-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                         EP512733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C3b binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR1-4 (266-274 KLKTQTNASD) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R28570,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R28570 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     334 knlrwtpyggcealccpepklnngeitghrksrpanhcvyf 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 sppacepnscinlpdiphaswetyprptkedvyvvgtvlryrchpgykpttdepttvicq 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 L-PSCEEKSCDN-PYIPNGDYS--PLRIK---HRTGDEITYQCRNGFYPAT-RGNTAKC- 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRP----YF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ptcekitcrkpdvshgemvsgfgplynykdtlvfkcqkgfvl--rgssvihcdadskwnp 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kpppdirngrhsge----enfyaygfsvtyscdprfsllghasisctvenetigvwrpsp 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAV--C-TESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                Hourcade D,
                                                                                                                                                                                                                                                                       91US-0695514
                                                                                                                                                                                                                                                                                                   92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                              266.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-9
/note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                . 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  510
                                                                                                                                                                                                                                                                                                                                                                               "ERTQRDKN substituted with KLKTQTNASD from SCR-8-9 to increase C3b binding"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543
                                                                                                                                                                                                              Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
            Annenkov A,
                                                                                                                           06-APR-1998;
                                                                                                                                                                                                                                                                     dystrophin; inflammatory response; interferon-gamma secretory response; autoimmune response; neurological response; Alzheimer's disease; Parkinson's disease; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
                                                                                            05-APR-1997;
                                                                                                                                                                                             WO9845430-A1
                                                                                                                                                                                                                                                                                                                                       Human; soluble complement receptor 1; sCR1; T-cell; B-cell; mediated immune response; inhibition; tissue rejection; gen
                                           (CHER/) CHERNAJOVSKY Y.
                                                                                                                                                            15-OCT-1998
                                                                                                                                                                                                                                                            Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of the soluble complement receptor 1 (sCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W73147 standard; protein; 778
                                                           (ANNE/) ANNENKOV A
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     positions in SCR-5-6 are substituted by amino acids from the corresponding positions in SCRs which are involved in C3b- and C4b-binding. The substitution variant given here has increased C3b-binding. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number R11810 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       279 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEYSERGDAYCTE-SGWRP-LPSCEEKSCDNPYIP-----NGDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaklktqtnsdfsp-----g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \tt RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                543 AA;
          Chernajovsky
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                          97GB-0006950
                                                                                                                           98WO-GB01012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 352.5; DB 1
Pred. No. 4.5e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 543;
                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is an amino acid sequence of the human soluble complement receptor 1 (SCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune response to prevent immune response-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         an interferon-gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed protein especially from cells that have been treated by gene therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fragment of soluble human complement receptor 1 - useful for treating T-cell or B-cell mediated immune responses e.g. inflammatory responses such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         epidermis bullosa or Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue rejection and destruction or clearance or inactivation of an
                 Cross-links
                                                                                                                       Membrane binding element; thrombotic disease; soluble protein; complement-related disease; integral membrane protein; inflammation; short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
                                                                                                                                                                                                                                                   30-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                       W45899 standard; peptide; 1930 AA
                                                                               Homo sapiens
                                                                                                                                                                                                           Human complememt receptor 1 (residues 1-1929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                           qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      778 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                 Location/Qualifiers 1930
/note= "Disulphide linked to Cys in peptide given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.7%; Score 350.5; DB 1 29.3%; Pred. No. 9.7e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal fragment. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 22; Pages 60-61; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-related and thrombotic diseases, providing improved localisation at cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0.1-10) mg/kg/day.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents human complement receptor 1 (CR1, CD 35)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-110524/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (ADPR-) ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-JAN-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably
                                                                                                                                                                  169
                                                                                 229
279 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                        270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                         60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                      DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                    WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                            -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                           cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                           wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                       RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg
                                                                                                                       YEYSERGDAYCTE-SGWRP-LPSCEEKSCDNPYIPN-----GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100;
                                                                               fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96GB-0014871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-EP03715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in W45889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith RAG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 350.5; DI
Pred. No. 2.9e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1930;
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                                                                                                                                                                            Matches
                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                       The invention relates to a human C3B/C4B receptor (CRI) protein. The CRI protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full-length human CRI as expressed on erythrocytes. The CRI function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-repersors the human cRI protein assays, and diagnostics. The present sequence
                   116
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                 -CR1 antibodies are used in assay represents the human CR1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYJO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 1A-P; 87pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cardiant activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A human C3B/C4B receptor (CR1) protein having antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Concino MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1974;
24-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5981481-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human C3b/C4b receptor (CR1) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y55751 standard; Protein; 2039 AA.
                                                   98
                                                                                                               43
                                                                                                                                                                                             Local
                                                                                                                                     3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG----
                                                                        RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                      cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd-
                                          -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1999-633357/54
                                                                                                                                                                              100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  condition;
                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV JOHNS HOPKINS
BRIGHAM & WOMENS HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Z38150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVANT
                                                                                                                                                                                                                                                      2039 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Carson
                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMUNOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74US-0350238.
93US-0026134.
88US-0176532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         89US-0332865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0470652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disorder; diagnostic.
                                                                                                                                                                                          18.7%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makrides SC, Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOSPITAL.
                                                                                                                                                                           55;
                                                                                                                                                                      Score 350.5; DB 20; Length 2039; Pred. No. 3.1e-18; 5; Mismatches 127; Indels 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fearon DT,
             -YKIEG
                                                                                                                                                                      Gaps
             168
                                                                                                           97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ip SH;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
                                This is full-length CR1 protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences. They are useful in diagnosing and treating immune disorders, and prevent
Sequence
                          perfusion injury.
                                                                                                                                                                          Claim 1; Fig 1; 191pp; English.
                                                                                                                                                                                                                 New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of complement-related immune defects,
                                                                                                                                                                                                                                                                    N-PSDB; N91477
                                                                                                                                                                                                                                                                               WPI; 1989-309498/42.
                                                                                                                                                                                                                                                                                                                                      (TCEL ) T CELL SCIENCES INC.
(UVJO ) THE JOHNS HOPKINS UNIVERSITY.
(BRIG ) THE BRIGHAM AND WOMEN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                   01-APR-1988;
                                                                                                                                                                                                       inflammation, myocardial infarct,
                                                                                                                                                                                                                                                                                                             Fearon DT, Klickstein
                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-OCT-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W08909220-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement; cotactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CR1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P92219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P92219 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    320 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN-----GDYSPLRIKHRTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg 269
2317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (human).
                                                                                                                                                                                                                                                                                                                                                                                                   88US-0176532
                                                                                                                                                                                                                                                                                                                                                                                                                                89WO-US01358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; 2317
                                                                                                                                                                                                                                                                                                           LB,
                                                                                                                                                                                                                                                                                                           Wong W,
                                                                                                                                                                                                       etc
                                                                                                                                                                                                                                                                                                          Carson G,
                                                                                                                                                                                                                                                                                                          Concino MF,
                                                                                                                                                                                                                                                                                                          Makrides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
                                                                                                                                                                                                                                                                                                          SC
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Query Match Best Local Similarity

18.7%; 29.3%;

Score 350.5; DB iv, Pred. No. 3.6e-18; "'Amatches 127;

DB 10; Length 2317;

Indels

59;

23;

Matches 100;

Conservative

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RESULT 10
R28557
XX R28557
AC R28557
AC R28557
XX R2950n
FT Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CR1-4 (99H, 103E) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R28557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R28557 standard; peptide; 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Ser substituted by His (SCR-9)" Misc-difference 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                   Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                     Atkinson JP,
                                                                                                                                                                                                                                                            (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                             28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EP512733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 329 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            163
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                              diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                 etc.
                                                                                                                                                                                                     Hourcade D,
                                                                                                                                                                                                                                                                                                                         91US-0695514.
                                                                                                                                                                                                                                                                                                                                                                                92EP-0303826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "TRUNCATED"
99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-2
451..510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= SCR-1
61..122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Thr substituted by Glu (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    269
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                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                        short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                    CR1-4 (52S, 53S, 54P) analogue
                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R28547 standard; peptide; 543 AA
Misc-difference
                                                         Region
                                                                                                                                    Region
                                                                                               Region
                                                                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligh-ssaeciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN-----GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/note= "TRUNCATED"
52
                                                       /label= SCR-8
511..543
                                                                                                   451..510
                                       /label= SCR-9
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                   /label= SCR-2
                                                                                                                                                      /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.5%; Score 347.5; DB 1
29.3%; Pred. No. 1.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    55; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                  169
                                                                                                                                                                                                                                    169
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                                                                                                                                                                                                                                                                                                             116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Gly substituted by Misc-difference 54
                                         279 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1992
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12
                                                                                                                                                                                                                                                                                                                                    56 drcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                        60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        2 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvw--sspk 55
                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diagnosis etc.
                                                                                                                                                    YEYSERGDAYCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG 269
                                                                                                                                                                                                               DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNNG 222
                                                                                                                                                                                                                                                             wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                   WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----
                                                                                                                                                                                        epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hourcade D, Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-0695514.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Thr substituted by Ser (SCR-8)"
53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Ala substituted by Pro (SCR-8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.4%; Score 345.5; DB 1 29.3%; Pred. No. 1.5e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SCR-8)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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R28560

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Дb
                                  QY
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                                                                                                                                                                                                              Matches
                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEO accoration number 501810 and Associations in the 1011-length CR1 amino acid sequence having GENESEO
                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                        accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1992-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR1-4 (114S) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R28560 standard; peptide; 543 AA
57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                               60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                 Local Similarity
                                                                                              3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                              cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                            543 AA;
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= SCR-1
61..122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Asp substituted by Ser (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= SCR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= SCR-2
                                                                                                                                           18.3%; Score 343.5; DB 1
29.0%; Pred. No. 2.1e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCR-9
                                                                                                                            56; Mismatches 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Krych M;
                                                                                                                                                           DB 13;
                                                                                                                              Indels
                                                                                                                                                           Length 543;
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RESULT
R28550
ID R28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CR1-4 (64K) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R28550 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
        The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain specified substitution variants of it are claimed in which certain
                                                                                                                                                  Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection.
                                                                                                                                                                                              WPI; 1992-375009/46
                                                                                                                                                                                                                       Atkinson JP,
                                                                                                                                                                                                                                                                                03-MAY-1991;
                                                                                                                                                                                                                                                                                                           28-APR-1992;
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                                                                                                                                                                                                                                                (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 wsnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
positions in SCR-2 which have been identified as important for the
                                                                                                            Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                       for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN-----GDYSPLRIKHRTG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= SCR-8
511..543
                                                                                                                                                                                                                         Hourcade D,
                                                                                                                                                                                                                                                                                91US-0695514
                                                                                                                                                                                                                                                                                                            92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             /note= "Arg substituted by Lys (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-1
                                                                                                                                                                                                                         Krych M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                          CR1-4 (85R, 87N) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                  R28553;
                                                                                                                                                                                                                                                                                                                                                                                                                                            R28553 standard;
                                                                                       /note= "Gln substituted by Arg (SCR-9)" Misc-difference 87
                                                                                                          /note= "TRUNCATED"
Misc-difference 85
                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1993 (first entry)
                                                                                                                                                               Region
                                                                                                                                                                                         Region
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                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            113 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
28-APR-1992;
                           11-NOV-1992.
                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           279 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 -rcrrkscknppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fvmkgprrvkcqalnkwepelpsc-srvcqpp--pdvlhaertqrdkdnfsp-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEMHC -- SDD -- GFWSKEKPKC - VEISCKSPDVINGSPIS - QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 AA;
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 92EP-0303826.
                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide; 543 AA.
                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                /note= "Lys substituted by Asn
                                                                                                                                                                             /label= SCR-8
                                                                                                                                                                                                                                 /label= SCR-1
                                                                                                                                                                                                         'label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18.2%;
29.0%;
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                                                                                                                                                     SCR-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 341.5; DB 
Pred. No. 3e-18;
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                                                                                 (SCR-9)"
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Best Local Similarity
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 short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                               CR1-4 (121Q) analogue
                                                                           19-MAR-1993
                                                                                                                             R28565 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                             279 qevfyscepg-ydlrgaasmrctpqgdwspaaptcevkscd 318
                                                                                                                                                                                                                                                                                                                              169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG 222
                                                                                                                                                                                                                                                                                                                                                         113 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1992-375009/46
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                                                                                                                                                                                                                         270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
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                                                                                                                                                                                                                                                                                                                                                                                                                                      60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis etc.
                                                                                                                                                                                                                                                                             YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                      epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv
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                                                                                                                                                                                                                                                                                                                                                                                                             -rcrrkscrnppdpvngmvhvikg--iqfgsrinysctkgyrligs-ssatclisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA;
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29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 13;
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       accession number R11810 and descriptions in the disclosure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complement activity regulator protein analogues - useful for treating auto: immune diseases, to suppress transplant rejection,
169 epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                   113 wdnetpicqripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1991;
                                                                                                                                   169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          543 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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Scoring table:
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  C4BP_BOVIN
CCPH_HSVSA
DAF_HUMAN
LEM3_MOUSE
LEM2_MOUSE
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DAF_PONPY
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LEM2_RAT
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APOH_BOVIN
LEM2_RABIT
F13B_MOUSE
HIG_DROME
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p20023 homo sapien
Q01339 mus musculu
p49457 pongo pygma
p05160 homo sapien
p16109 homo sapien
p98109 ovis aries
Q60401 cavia porce
p98105 rattus norv
p33730 canis famil
p17690 bos taurus
p27113 orryctolagus
Q07968 mus musculu
Q09101 drosophila
Q61475 mus musculu
p02749 homo sapien
Q61476 mus musculu
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P04003 homo sapien
P10998 vaccinia vi
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297	270	372	372	372	372	372	372	372	646	345	485
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APOH_RAT	CFHE_HUMAN	LEM1_PAPHA	LEM1_MACMU	LEM1_RAT	LEM1_PONPY	LEM1_PANTR	LEM1_HUMAN	LEM1_MOUSE	LEM3_BOVIN	APOH_CANFA	LEM2_BOVIN
P26644 rattus norv	P36980 homo sapien	Q28768 papio hamad	Q95198 macaca mula	P30836 rattus norv	Q95235 pongo pygma	Q95237 pan troglod	P14151 homo sapien	P18337 mus musculu	P42201 bos taurus	P33/03 canis ramii	P98107 bos taurus

ALIGNMENTS

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C1 P- = Z Z S5-	SEQUENCE OF 19-35. SEQUENCE OF 19-35. SIM R.B., Disciplo R.G.; "Purification and structural studies on the complement-system control protein beta 1H (Factor H)."; Biochem. J. 205:285-293(1982).		Eur. J. [3] SEQUENCI MEDLINE Kristens "Structu binding J. Immu	SEQUENCE FROM N.A. TISSUE=LIVER; MEDLINE; 88134059. Ripoche J., Day A.J., Harris T.J.R., Sim R.B.; "The complete amino acid sequence of human complement factor H."; Biochem. J. 249:593-602(1988). [2] [2] [2] [2] [2] SEQUENCE OF 53-445 FROM N.A. MEDLINE; 87054207. Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F., Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.; Schulz T.F. Schwaeble W., Stanley K.K., Weiss E., Dierich M.P.;	RESULT 1 CFAH_HUMAN CFAH_HUMAN TANDARD; PRT; 1231 AA. AC P08603; DT 01-AN-1990 (Rel. 08, Created) DT 01-AN-1990 (Rel. 13, Last sequence update) DT 30-MAY-2000 (Rel. 3), Last annotation update) DE COMPLEMENT FACTOR H PRECURSOR. GN HF1 OR HF OR CFH. OS HOMO Sapiens (Human). CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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11. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

12. SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.

13. CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 9233649.

Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.;

"Solution structure of the fifth repeat of factor H: a second example of the complement control protein module.";

Biochemistry 31:3626-3634(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [8]
STRUCTURE BY NMR OF 866-985 (SUSHIS 15 AND 16).
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STRUCTURE BY NMR OF 264-322 (SUSHI 5).
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IBL; X04697; CAB41739.1; ALT_FRAME.

IBL; M55294; AAA35948.1; -.

IR; S00254; NBHUH.

IR; S00254; S00254.

IR; S03013; S03013.

IR; S1HCC; 15-APR-92.

IHCC; 15-APR-92.

IHCC; 15-APR-92.

IHCC; 15-APR-93.

IB; 11FF; 15-JUL-93.

IB; 11FF; 15-JUL-93.

IB; 11F7; 15-JUL-93.
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                                                                                                                                          Steinkasserer A., Norman D.G., Kieffer B.,
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871 891 891 891 891 891 894 900 904 907 904 907 904 907 918 920 926 8A; 139125 MW; C65EC8CF8800B3FD CRC64;
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01-JAN-1988 (Rel. 06, Last sequence update)
01-VOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT FACTOR H PRECURSOR (PROTEIN BETA-1
                                                                                                                                      This SWI
between
                                                                                                                                                                                                                                                             "Demonstration of an unusual allelic variation of the complete cDNA sequence of the H.2 allotype."; J. Inmunol. 144:358-362(1990); -i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN
                                                                                                                                                                                                                                                                                                                                                                               Munoz-Canoves P., Tack B.F., Vik D.P.; "Analysis of complement factor H mRNA (IFN-gamma increase the level of H in L Biochemistry 28:9891-9897(1989).
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            EMBL; M12660; AAA37759.1; -. EMBL; J02891; AAA37795.1; -. EMBL; M31979; AAA37762.1; -.
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the European Bioinformatics Institute. There are no restrictions
use by non-profit institutions as long as its content is in
modified and this statement is not removed. Usage by and for con
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POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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MGD; MGI:88385; CFH.
INTERPRO; IPR000436;
PFAM; PF00084; sushi;
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P04003;
23-OCT-1986 (Rel. 02, C)
01-OCT-1993 (Rel. 27, L)
01-NOV-1997 (Rel. 35, I)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.; "Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein."; Biochem. Biophys. Res. Commun. 165:138-144(1989).
                                                                            MEDLINE;
                                                                                                                                                                                                                         Lintin S.J., Lewin A.R., Reid K.B.M.; "Derivation of the sequence of the signal peptide in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE; 91113199.
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CARBOHYD
           Intin S.J., Reid K.B.M.; "Studies on the structure of the human C4b-binding protein gene.";
                                                                                                  SEQUENCE OF 203-288 FROM N.A.
                                                                                                                                                                                                                                                                                             MEDLINE; 88242821
                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 9-81 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Aso T.,
                                                                                                                                                                                                                                                                                                                                                                                                  ASO T., Okamura S., Matsuguchi T., Sakamoto N., Sata T., Niho Y.; "Genomic organization of the alpha chain of the human C4b-binding protein gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
MEDLINE; 9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4BPA OR C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4B-BINDING
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Lett.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPFCEEKRCSPPYILNGIYTPHRI 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW
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                                                                            86301119
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204:77-81(1986)
                                                                                                                                                     232:328-332(1988).
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(Rel. 35, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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67.0%;
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Pred. No. 4.9e-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
MW; C5AC02F341B957F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                      174:222-227(1991).
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TYPESTATION DEPOCHMENT OF THE CALL MACHINE TO THE COMPLEXES WITH RT VICIAL REGISTRATION OF HUMBAN CASE STATE CLASSICAL PARTHWAY OF COMPLEMENT PROCESS OF THE CLASSICAL PARTHWAY OF COMPLEMENT CC ACTIVATION. IT BINDS AS A COFACTOR TO C39/C4B INACTIVATOR CC ACTIVATION. IT BINDS AS A COFACTOR TO C39/C4B INACTIVATOR CC ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3) CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C4B. IT COMPLEXACTS ALSO WITH ANTICOAGULANT PROTEIN S CC CALM BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CC CALM BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CC CALM BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CC CAND WITH SERUM AMYLOID P COMPONENT.

CC INDUST: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF A SOO KDA COMPLEX OF A POSSIBLE SORTS: A 570 KDA COMPLEX OF 7 ALPHA CHAINS OR D 1 BETA CHAIN A 530 KDA HOMOHEPTAMER OF ALPHA CHAINS OR A 500 KDA COMPLEX OF A ALPHA CHAIN AND HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE CITISUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.

CC I- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.

CC -- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

CC -- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                     EMBL;
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                                                                MIM; 120830;
                                                                                               EMBL; X02865; CAA266
PIR; A33568; NBHUC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chung L.P., Gagnon J., Reid K.B.M.; "Amino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chung L.P., Bentley D.R., Reid K.B.M.;
"Molecular cloning and characterization of the cDNA coding for C4b-
binding protein, a regulatory protein of the classical pathway of the
human complement system.";
Biochem. J. 230:133-141(1985).
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SEQUENCE OF 80-597 FROM N.A.
MEDLINE; 86025405.
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                                                                                                                             M62476; AAA36506.1;
M62477; AAA36506.1;
M62479; AAA36506.1;
M62480; AAA36506.1;
M62481; AAA36506.1;
M62482; AAA36506.1;
M62482; AAA36506.1;
M62482; AAA36506.1;
M62484; AAA36506.1;
M62484; AAA36506.1;
M62484; CAA37839.1;
M62484; CAA37839.1;
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M62486; AAA36506.1;
M62475; AAA36506.1;
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                            IPR000436; -.
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                                                                                                                 CAA26617.1;
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Complement

pathway;

Plasma; Glycoprotein; Repeat; Sushi; Signal;

PFAM; PF00084; sushi;

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P10998;
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COMPLEMENT
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                                                                                                                   PTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVL--RGSSVIHCDADSKWNP
                                                                                                                                    PKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAV--C-TESGWRP
                                                                                                                                                                     LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                      FTLTGGNV-----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC 128
                                                                                                                                                                                                                       TETRFKTGTTLKYTCLPGYYRSHSTQTLTCNSDGEWV-YNTF--CIYKRCRHPGE----- 118
                                                                                                                                                                                                                                      SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                   SPPACEPNSCINLPDIPHASW 310
                                                                                                                                                     KPPPDIRNGRHSGE----ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSP
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9 (Rel. 11, Created)
9 (Rel. 11, Last sequence update)
8 (Rel. 36, Last annotation update)
8 (Rel. 36, Last annotation update)
7 CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN 35)
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2399
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30.7%;
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IHSUS
IHSUS
                                                                                                                                                                                                                                                                Score 303; DB 1;
Pred. No. 1.5e-17;
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; 67E03F2EA85A16DD CRC64;
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8 X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                     INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                           /FTId=VAR_001977
                                          PRT;
                                                                                                                                                                                                                                                         Mismatches
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                                          263
                                                                                                                                                                                                                                                                                                                                          (GLCNAC...).
                                                                                                                                                                                                                                                                                                                                                           (GLCNAC.
                                          A
                                                                                                                                                                                                                                                         101;
                                                                                                                                                                                                                                                                         Length 597;
                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          38;
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                      231
                                                                                                                                                                                                                                                          16;
 EMBL; X13166; CAA31564.1; -
EMBL; M22812; AAA69605.1; -
EMBL; M35027; AAA7997.1; -
PIR; A31005; WMVZSP.
PDB; 1VVC; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PROTEIN C3) (28 KDA PROTEIN). C3L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 88318974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                      Goebel S.J., Johnson G.P., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                       Goebel S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-WR;
                                                                                                                                                                                                                                                                                                                                                      STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                               Virology
                                                                                                                                                                                                                                                                                                                                                                                                Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                  Barlow P.N.;
                                                                                                                                                                                                                          Wiles A.P., Shaw G.,
                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                           STRUCTURE
                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                             Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                               COMPLETE GENOME
                                                                            entities requires
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                                                                                                                                                                                                                                                                                                                                                                                                                91021027.
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                                                                                                                                                                                                                                           BY NMR OF 146-263.
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Kotwal G.J., Moss B.;
"Vaccinia virus encodes a secreto:
to complement control proteins.";
Nature 335:176-178(1988).
[2]
                                                                                                                                                                                                                                                                                                                                              COMPLEMENT ACTIVATION.";

COMPLEMENT ATTACK

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COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

COMPLEMENT ACTIVATION BINDS C3B AND C4B.

COMPLEMENT ACTIVATION (RCA).

COMPLEMENT ACTIVATION (RCA).
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kotwal G.J., Moss B.;
"Analysis of a large cluster of nonessential
vaccinia virus terminal transposition mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 92115714.

ISAACS S.N., Kotwal G.J., Moss B.;

"Vaccinia virus complement-control protein prevents
antibody-dependent complement_enhanced neutralization of infectivity
                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and contributes to virulence."
                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "NMR studies of a viral protein that mimics the regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complete DNA sequence of vaccinia virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natl. Acad. Sci. U.S.A.
; CAA31564.1; -.; AAA69605.1; -.
                                                                                                                                             a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        G.P., Perkus M.E., Davis S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bright J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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Best Local
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                repeating domains that are composed of the short consensus characteristics of C3/C4 binding proteins."; J. Exp. Med. 165:1095-1112(1987).
                                                                                Klickstein L.B., Wong W.W., Smith J.A., Weis J.H., Wilson J.G., Fearon D.T.;
                                                                                                                                                      Fearon D.T.;
"Identification of distinct C3b and human C3b/C4b receptor (CR1, CD35) b
J. Exp. Med. 168:1699-1717(1988).
                                                                                                                MEDLINE;
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                                                            "Human C3b/C4b receptor (CR1). Demonstration of long homologous
                                                                                                                           SEQUENCE OF 503-2039 FROM N.A.
                                                                                                                                                                                                                   Klickstein L.B., Bartow T.J., Miletic V.,
                                                                                                                                                                                                                                   MEDLINE; 89035992
                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   Mammalia;
                                                                                                                                                                                                                                                                                                Eukaryota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISNGR--HNGYED--FYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-DPPTCQIVKCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFN----QCIKRRCPSPRDIDNGQ 96
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4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 301.5; DB 1
Pred. No. 7.9e-18;
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                                                                                                                                                                    by deletion mutagenesis.";
                                                                                                                                                                                   C4b recognition sites in the
                                                                                                                                                                                                                 Rabson L.D.,
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EMBL; M11617; AAA52298.1; --
EMBL; M11618; AAA52299.1; --
EMBL; Y00816; CAA68755.1; --
EMBL; X05309; CAA28933.1; --
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PIR; C24748; C24748.
PIR; S03843; S03843.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong W.W., Klickstein L.B., Smith J.A., Weis J.H., Fearon D.T.;
"Identification of a partial cDNA clone for the human receptor for
complement fragments C3b/C4b.";
Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).
-I- FUNCTION: CR1, PRESENT ON ERYTHROCYTES, LEUKCCYTES, GLOMERULAR
PODOCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE
BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERPRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER.

SUBUNIT: MONOMER.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.

POLYMORPHISM: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A

MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A

LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A

CONTAINED A SITE DEFERMINING C4 SPECIFICITY, AND THE N-TERMINAL

TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE OF CRI. SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
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B24748; B24748.
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een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000436; -
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Sushi; Blood group
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7 X SUSHI
REPEAT C.
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Q1-NOV-1997
Q1-NOV-1997
15-JUL-1998
C4B-BINDING
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MEDLINE; 97166082.
Hillarp A., Wiklund H.
                                                                            SEQUENCE FROM N.A
 Hillarp A., Wiklund H., Thern
Molecular cloning of rat C4b
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ia; Eutheria; Rode
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR.
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                                                           TISSUE-LIVER;
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Pred. No. 1.4e-16;
Prematches 111;
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J. Immunol. 158:1315-1323(1997)
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     17
                     PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEW---VALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R. SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SERUM AMYLOID P COMPONENT.
PPPDLPYALPASEMNQTDFESHTTLRYNCRPGYSRASSSQSLYCKPLGKWQINIA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR000436; -
                                               Conservative
                                                          18.5%;
                                                                                                           62266 MW;
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                                                43;
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SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 6.
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                                              Score 276.5; DB
Pred. No. 2e-15;
3; Mismatches 1
                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . . .) (POTENTIAL).
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                                               104;
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BETA CHAIN) (POTENTIAL).
                                                                    Length 558;
                                              Indels
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REPEAT REPEAT

57 57 119 1180 180 244 302 358

SUSHI SUSHI SUSHI IHSUS

SUSHI

6 X SUSHI (SCR) REPI SUSHI (SCR) REPEATS

BY SIMILARITY.

REPEAT REPEAT

DISULFID REPEAT

REPEAT

CHAIN

DOMAIN

SIGNAL

MGD; MGI:88229;

C4BP.

PF00084; sushi;

Plasma;

Glycoprotein; Repeat; Sushi;

IPR000436; -. pathway;

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C4BP_MOUSE
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01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                  EMBL; M17122; AAA37312.1;
                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                        PIR; A27117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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 Cervoni F., Fenichel P.,
                                                                          Lublin D.M., Liszewski M.K., Post T.W., Arce M.A., le Beau M.M., Rebentisch M.B., Lemons R.S., Seya T., Atkinson J.P.; "Molecular cloning and chromosomal localization of human membrane cofactor protein (MCP). Evidence for inclusion in the multigene
                                                                                                                         SEQUENCE FROM N.A., AND SEQUENCE OF 35-58 MEDLINE; 88286080.
                                                                                                                                                                                                                    MEMBRANE
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01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                            Mammalia;
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             MEDLINE; 93119658
                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                          TESG-WRPLPSCEEKSCD-NPYIPNGDYSPL 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AKKHCRNPGYLDNG---YVNGETITFGSQIEFSCQEGFILVGS-STSSCEVRGKGVAWSN 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTN 118
                                                                                                                                                                                                                                                                                                                                    QGNGNWSSLPTC-EFDCDLPPAIVNGYYTSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS--- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPPAIPNALPASDVNRTDFESHTTLKYECLPGYGRGISRMMVYCKPSGEWEISVS----C 115
                                                                                                                                                                                                                                                                                                                                                                                 KTVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVIEC
                                                                                                                                                                                                                                                                                                                                                                                                        -DDGFWSKEKPKCVEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVC
                                                                                                                                                                                                                    COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST
                                                                                                                                                           ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                         COMMON ANTIGEN) (TLX).
                                                        complement-regulatory proteins."; ed. 168:181-194(1988).
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  Akhoundi C.,
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EMBL; Y00651; CAA68675.1; EMBL; S51940; AAB24802.1; EMBL; M58050; AAA62833.1; EMBL; A18585; CAA01400.1; EMBL; S65879; AAD13968.1; PIR; S01896; S01896.

HSSP; P10998 MIM; 120920;

P10998; 1VVC

INTERPRO; IPR000436;

PF00084; sushi; 4.
ement pathway; Glycoprotein; Transmembrane; Repeat; Signal;

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-1- FUNCTION: MCP IS AN IMPORTANT MEMBRANE PROTEIN FOR PROTECTING HOST CELLS FROM DAMAGE BY COMPLEMENT. MCP POSSESSES COFACTOR ACTIVITY FOR INACTIVATION OF C3B AND C4B BY SERUM FACTOR I. THIS WOULD ALLOW MCP TO REGULATE THE COMPLEMENT SYSTEM AT THE LEVEL OF THE C3 CONVERTASES, MAY BE INVOLVED IN THE FUSION OF THE SPERMATOZOA WITH THE OCCYTE DURING FERTILIZATION. MAY ACT BY PREVENTING COMPLEMENT ACTIVARION AT THE FETO-MATERNAL INVERFACE ON THE SPERMATOZOA WITH SYNCYTIOTROPHOBLAST LAYER OF PLACENTA.

-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-1- ALTERNATIVE PRODUCTS: AT LEAST 14 FORMS ARE PRODUCED BY ALTERNATIVE SPLICING. THE FORM SHOWN IS THE TRANSCRIPT A. THE GAMMA ISOFORM (TRANSCRIPTS A AND B) IS PREFERENTIALLY EXPRESSED IN EBU-B CELLS AND LEUKEMIC CELLS. THE 66 KDA ALPHA ISOFORM AND THE EBY-B CELLS AND LEUKEMIC CELLS. THE 65 KDA ALPHA ISOFORM FOUND IN ALL TISSUES EXCEPT SPERM CORRESPOND TO THE TRANSCRIPTS C AND D, AND THE TRANSCRIPTS A DOFF RESPECTIVELY. THE EXON 9 IS SPECIFICALLY DELETED IN SOME PLACENTAE. THE EPSILON ISOFORM CORRESPONDS TO THE TRANSCRIPTS I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i-
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a membrane cofactor protein like genetic element.";
                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 1-34 FROM N.A. MEDLINE; 94014356.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cofactor protein (MCP, CD46)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Tissue-specific and allelic expression of the complement regulator CD46 is controlled by alternative splicing.";
Eur. J. Immunol. 22:1513-1518(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Characterization of a cDNA clone coding for human testis membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 92289809
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - i - PTM: EXTENSIVELY O-GLYCOSYLATED IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunol. 151:4137-4146(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 AND 13. ALL TISSUES DIFFERENTIALLY SPLICE EXON 13.
TISSUE SPECIFICITY: EXPRESSED BY ALMOST ALL CELLS EXCEPT
ERYTHROCYTES AND SOME BONE MARROW CELLS.
                                                                                                                                                                                                                                                                                                            SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD46 entry:
WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD46.HTM".
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01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
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                                                                                                                                                                                                                                                                                                   DGSDTIVCDSNSTWDPPVPKC
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SUSHI 3.
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BY SIMILARITY
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Pred. No. 2.1e-15;
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VARIANT ARG-149.
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MEDLINE; 991345U8.

YE S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupta R.;

"A PstI polymorphism detects the mutation of serine-128 to arginine
CD 62E gene - a risk factor for coronary artery disease.";

J. Biomed. Sci. 6:18-21(1999).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
MEDLATES THEIR BINDING TO LEUKOCYTES. THE LICAND RECOGNIZED BY
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                         Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schattke S., Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A.; "E-selectin polymorphism and atherosclerosis: an association study."; Hum. Mol. Genet. 3:1935-1937(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Bu "Insight into E-selectin/ligand interaction from the crystal structure and mutagenesis of the lec/EGF domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 367:532-538(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ligand, sialyl-Lex.";
Science 250:1130-1132(1990).
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Hakomori S., Paulson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils related to complement regulatory proteins and lectins.", Science 243:1160-1165(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3D-STRUCTURE MODELING OF LECTIN DOMAIN
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       GLYCOLIPIDS).

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH A HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH AN ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN
  UNSELECTED POPULATION
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Primates;
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(SER-149).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87:1673-1677(1990)
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INTERPRO; IPRO00436;
INTERPRO; IPRO00561;
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PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS00615; C_TYPE_LECTIN_2; 1.
Cell adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A38615; A38615.
PDB; 1ESL; 31-AUG-94.
PDB; 1KJA; 03-APR-96.
MIM; 131210; -.
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD62E entry:
WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD62E.HTM".
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ## M30640; AAA52377.1; -
## M61893; AAA52375.1; -
## M61895; AAA52375.1; J
## M61887; AAA52375.1; J
## M61888; AAA52375.1; J
## M61890; AAA52375.1; J
## M61891; AAA52375.1; J
## M61891; AAA52375.1; J
## M61892; AAA52375.1; J
## M61892; AAA52376.1; -
## M24736; AAA52376.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                        A32606; A32606.
A35046; A35046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                      PF00059; lectin_c; 1. PF00084; sushi; 6.
                                                                                                                                                                                                                                                                                                                                                         PF00008; EGF;
                                                                                                                                                                                                                                                                       Signal;
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139
179
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429
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111
143
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367
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JOINED.
                                                                                                                                      POTENTIAL.

CYTOPLASMIC (POTENTIAL).

C-TYPE LECTIN (SHORT FORM).

EGF-LIKE.

6 X SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 4.

SUSHI 6.
                                                                                                                                                                                                                                           E-SELECTIN.
EXTRACELLULAR (POTENTIAL)
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⟨ SIMILARITY

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CARBOHYD
                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE A
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CARBOHYD
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SEQUENCE FROM N.A.
TISSUE-AORTIC ENDOTHELIUM;
MEDLINE; 94271236.
Tsang Y.T.M., Haskard D.O.,
                                                                                     MEDLINE; 95071392.
Rollins S.A., Evans M.J.,
                                                                                                             SEQUENCE FROM N.A.
TISSUE=AORTIC ENDOTHELIUM;
                                                                                                                                                                                                                                             P98110;
                                                                                                                                                     Eukaryota;
                                                                                                                                                              Sus scrofa
                                                "Molecular and functional analysis of porcine E-selectin potential role in xenograft rejection."; Biochem. Biophys. Res. Commun. 204:763-771(1994).
                                                  potential role in xenograft re
Biochem. Biophys. Res. Commun.
                                                                                                                                            Mammalia;
                                                                                                                                                                                 (CD62E).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRK---CQ--KRP-----CGHP
                                                                                                                                                                                                                                                                                                                                                                                                  PVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                GDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCL 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SFPWNTTCTFDCEEGFELMGAQSLQCTSSGNWDNEKPTCKAVTCRAVRQPQNGSVRCSH-
                                                                                                                                                                                                                                                                                                                                                VRC---DAVHQPPKGLVRCAHSPIGE-FTYKSSCAF--SCEEGFELHGSTQLECTSQGQW
                                                                                                                                                                                                                                                                                                                                                                   ISCKSPDVIN------GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-W
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                                                                              L.A., Rother R.P.;
                                                                                                                                            Eutheria;
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Metazoa;
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27.1%;
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                                                                                          Johnson K.K.,
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CAD).
  Robinson M.K.;
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H -> Y (IN REF. 2)
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ADHESION MOLECULE 2) (LECAM
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                                                                                           Squinto S.P.,
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PROSITE;
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PFAM; PF00059; lectin_c; 1.
PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO;
INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDLED EUROCYTES. THE LIGAND RECOGNIZED BY ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES OF POLYLACTOSSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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INTERPRO; IPR000561; -.
INTERPRO; IPR001304; -.
INTERPRO; IPR002396; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U08350;
HSSP; P16581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and expression kinetics of porcine vascular cell adhesion molecule.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR ALLOGRAFT REJECTION AND PROBABLY ALSO IN XENOGRAFT REJECTION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS; PORCINE E-LECTIN LACKS

THE HUMAN SUSHI-1 AND -4 EQUIVALENTS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restably non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PR00343; SELECTIN.

5; PS00072; EGF_1; 1.

5; PS01186; EGF_2; 1.

6; PS00615; C_TYPE_LECTIN_1; 1.

6; PS50041; C_TYPE_LECTIN_2; 1.
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BY SIM
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                                                                                                                  Y SIMILARITY
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C4BP_BOVIN
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C4BP_BOVIN

C4BP_BOVIN

C2BP_505;

T 01-NOV-1997 (Rel. 35, Created)

T 01-NOV-1997 (Rel. 35, Last sequence update)

O1-NOV-1997 (Rel. 35, Last annotation update)

AR-BINDING PROTEIN ALPHA CHAIN PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QΥ
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the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                              Hillarp A., Thern A., Dahlbaech B.;

"Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains provides structural background for lack of complex formation with protein S.";

J. Immunol. 153:4190-4199(1994).

-I- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM ANYLOID P COMPONENT.

-I- SUBUNIT: DISSILFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Eukaryota; Metazoa;
Mammalia; Eutheria;
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 LEVPREINMSCSGEPVFGAVC-----TFACPEGWMLNGSVALTCGATGHWSGMLPTCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         195 PDV-----INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WR-PLPSCE 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     196 QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQN---GD 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                       (BY SIMILARITY).
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
                                             SWISS-PROT entry is copyright. It is produced through a collable een the Swiss Institute of Bioinformatics and the EMBL outst European Bioinformatics Institute. There are no restrictions
                                                                                                                         SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VSCNHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KNG-LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSS
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27.1%;
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N-LINKED (GLCNAC. . .) (POTENTIAL)
C -> Y (IN REF. 2).
L -> F (IN REF. 2).
T -> N (IN REF. 2).
K -> N (IN REF. 2).
V -> A (IN REF. 2).
V -> M (IN REF. 2).
KFYPSSSSECLOPNGSYOMPSDLI ->
NLFLPAAPNAFYPMDPTYCLLT (IN REF. 2).
MW; AFF74FE2SC1FD013 CRC64;
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2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 266;
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l.2e-14
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CARBOHYD
CCPH_HSVSA
Q01016;
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                                                               -- EGDSLIHCEADNSWNPPPPTCELNGCLGLPHIPH
                                                                                                                                             WSDPLPQCIIAKCEPPPTISNGR--HNGGDED-FYTYGSSVTYSCDRDFSMLGKASISCR
                                                                                                                                                                WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS
                                                                                                                                                                                      KKRCENPGE-----LLNGQVIVKTDYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVV
                                                                                                                                                                                                                                                  LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQ 63
                                                                                 SERGDAV -- C-TESGWR-PLPSCEEKSC-DNPYIPN
                                                                                                                                                                                                        KRPCGHPGDTPFGTFTLTGGNV-----FEYGVKAVYTCNEGYQLLGEIN-YRECDTDG--
                                                                                                                                                                                                                              IPPYLDFAFPINELNETRFETGTTLRYTCRPGYRISSRKNFLICDGTDNW----KYKEFCV 108
                                                                                                      VENKTIGVWSPSPPSCKKVICVQPVVKDG----
                                                                                                                          DD---
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P10998; 1VVC.
                                                                                                                                                                                                                                                                                 Similarity
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          STANDARD;
                                                                                                                                                                                                                                                                                                                        Plasma;
                                                                                                                                                                                                                                                                                17.7%;
27.5%;
                                                                                                                                                                                                                                                                                                                    MA; Glycoprotain; Repeat; Sushi; Signal.

BY SIMILARITY.
C4B-BINDING PROTEIN ALPHA CHAIN.

8 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 1.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 8.
BY SIMILARITY.
B
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                                                                                                                                                                                                                                                                       45;
                                                                                                                                                                                                                                                                      Score 265.5; DB 1
Pred. No. 1.8e-14;
5; Mismatches 110
          PRT;
          360
                                                                                                      KITSGFGPIYTYQQSIVYACNKGFRL
          ₽
                                                                                  256
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                                                                                                                                                                                                                                                                       110;
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                                                                                                                                                                                                                                                                                            610;
                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                      161
                                                                                                      273
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          [2]
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MEDLINE; 92260674.

Albrecht J.-C., Fleckenstein B.;

Albrecht J.-C., Fleckenstein B.;

New member of the multigene family of complement berpesvirus saimiri.";

J. Virol. 66:3937-3940(1992).

-!- ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND ALTERNATIVE SPLICING OF THE SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE COMPLEMENT ACTIVATION (RCA).

-!- SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X64346; CAA45626.1; -.
EMBL; X64346; CAA45627 1; -.
EMBL; X60283; CAA42823.1; -.
EMBL; X60283; CAA42822.1; -.
PIR; B42534; WMBELE.
PIR; A42534; WMBELE.
PIR; S24567; S24567.
HSSP; P10998; 1VVC.
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01-APR-1993 (Rel. 2)
15-JUL-1998 (Rel. 3)
COMPLEMENT CONTROL I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal; Repeat
Glycoprotein.
SIGNAL
                                                                                                                                                                                                                       DISULFID
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DISULFID
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TRANSMEM
DISULFID
DISULFID
DISULFID
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CARBOHYD
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DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammaherpesvirinae;
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Viruses; dsDNA
  SEQUENCE
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01-AUG-1988 (Rel. 08, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR (CD55).
                                                        GPI-ANCHOR.
  Moran P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning and characterization of cDNAs encoding the complete sequence of decay-accelerating factor of human complement.";
                          MEDLINE;
                                                                                                   Biochim.
                                                                                                                                                                                    Nakano Y., Sugita
                                                                                                                                                                                                         MEDLINE; 91291869.
                                                                                                                                                                                                                                                            SEQUENCE OF 35-46.
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Leykam J.F., Atkinson J.P., Tykocinski M.L.:
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                                                                                                                                                         'Isolation of two forms
                                                                                                                                                                                                                                                                                                                                                                                              Ewulonu U.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-100 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 6-381 FROM N.A. (DAF-2 FORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning of decay-accelerating factor suggests novel use of splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nussenzweig V.;
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U.K., Ravi L.,
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Primates;
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                                                                                                                                                                              Ishikawa Y., Choi N.-H.,
                                                                                                   1074:326-330(1991)
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                                                                                                                                                         o f
  W.J.,
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                                                                                                                                                   decay-accelerating factor (DAF) from human
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Pred. No. 1.2e-14;
2; Mismatches 119;
Caras I.W.
                                                                                                                                                                                                                                                                                                             88:4675-4679(1991)
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Catarrhini;
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                                                                                                                                                                              Tobe T., Tomita M.;
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between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us

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C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION.

INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF THE COMPLEMENT CASCADE.

-I- FUNCTION: ALSO ACTS AS THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED VIBUSES (ECHOVIRUSES 13, 21, 29 AND 33).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    decay-accelerating factor in Cromer blood group phenotypes.";
Blood 84:1276-1282(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakano Y., Sumida K., Kikuta N., Miura N.-H., Tobe T., Tomita M.; "Complete determination of disulfide bonds localized within the short consensus repeat units of decay accelerating factor (CD55 antigen)."; Biochim. Biophys. Acta 1116:235-240(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lublin D.M., Mallinson G., Poole J., Reid M.E., Tho
Ferdman B.R., Telen M.J., Anstee D.J., Tanner M.J.A
"Molecular basis of reduced or absent expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT BLOOD GROUP DR(A-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBO J. 13:5070-5074(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Almond J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ward T., Pipkin P.A., Clarkson N.A., Stone D.M., Minor P.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFIDE BONDS IN SUSHI DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biol. Chem. 266:1250-1257(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [6]
                                                                                                                                                                                                                                                                                                                                                                                                                     PTM: THE SER/THR-RICH DOMAIN IS HEÁVILY O-GLYCOSYLATED.
POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROWER BLOOD GROUP
SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-INCIDENCE (CR(A),
TC(A), DR(A), ES(A), WES(B), UMC, AND IFC, AND LOW-INCIDENCE
(TC(B), TC(C), AND WES(A)) ANTIGENS THAT RESIDE ON DAF. IN THE
CROMER PHENOTYPES DR(A-), AND INAB THERE IS REDUCED OR ABSENT
EXPRESSION OF DAF, RESPECTIVELY. IN THE CASE OF THE DR(A-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR. ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA COMPLEMENT PROTEINS. IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS LINING EXTRACELLULAR COMPARTMENTS, AND VARIANTS OF THE MOLECULE ARE PRESENT IN BODY FLUTUS AND IN EXTRACELLULAR MATRIX.

DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR
                                               DATABASE: NAME=PROW;
                                                                                                                              SIMILARITY: BELONGS
                                                                                                                                                                              SIMILARITY: CONTAINS
                                                                                                                                                                                                                                                        PHENOTYPE, A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION THAT IS THE BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS
WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD55.HTM"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE ACTIVE SITE ON SCR3 (BY SIMILARITY).
                                                                                           (RCA) FAMILY.
                                                                                                                                                                                                                         PHENOTYPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92305034.
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TO THE
                                           NOTE=CD guide CD55 entry;
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                                                                                                                                                                              SUSHI (SCR) REPEATS
                                                                                                                                  RECEPTORS
                                                                                                                                  OF COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thompson E.S.
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EMBL;
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DOMAIN
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complement pathway; Plasma; Glycoprotein; Membrane;
Alternative splicing; GPI-anchor; Signal; Sushi; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P08603; 1HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                  VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LIPID
                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                               CONFLICT
207
                              114 DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                   152
                                                                                                     54
                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A26359; A26359.
; S16187; S16187.
; A39101; A39101.
; S23138; S23138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L; M31516; AAA52169.1; -.
L; M30142; AAA52168.1; -.
L; M5799; AAA52167.1; -.
L; M64653; AAA52170.1; -.
L; M64356; AAA52170.1; JOIN
L; S72858; AAC60633.1; -.
L; B36359; B26359.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125240;
                                                                                                     VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
SGSSYQWSDPLPECREIYC-----PAPPQIDNGIIQGERDHYGYRQSYTYACNKGFTMIG
                                                                                                                                      EFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKW 153
                                                                                                                                                                       EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                   --STAVEFCKKKSCPNPGEIRNGQIDVPGGILF--GATISFSCNTGYKLFGSTS-SFCLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group antigen.
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                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                               381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          splicing; GPI-anchor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                  227
                                                                                                                                                                                                                                                                                                                                                                                                   199
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85
                                                                                                                                                                                                                          17.5%;
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                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REMOVED IN
4 X SUSHI
                                                                                                                                                                                                                          Score 262; DB 1
Pred. No. 2e-14;
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                                                                                                                                                                                                                                                                                                                                                /FTId=VAR_002000.
A -> P (IN CR(A-) ANTIGEN)
/FTId=VAR_002001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSRTPGFKRSFHFSLPSSWYYRAHVFHVDRFAWDASNHGLA DLAKEELRRKYTQVYRLFLVS (IN ISOFORM DAF-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTCFTLTGLLGTLVTMGLLT -> SRPVTQAGMRWCDRSSL
                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR_001999.
S -> L (IN DR(A-) ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId=VAR_001998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /FTId=VAR_001997
                                                                                                                                                                                                                                                                                                               -> I (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                   -> R (IN WES(A) ANTIGEN).
                                                                                                                                                                                                                                                                                                29138EEB6B4B565E CRC64;
                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (IN TC(C) ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (IN TC(B) ANTIGEN).
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                                                                                                                                                                                                                                          DB 1; Length 381;
                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polymorphism;
                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat
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LEM3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
(CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. Expression of both
and P-selectin is inducible by tumor necrosis factor alpha.";
J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SELP OR GRMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q01102;
                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a continuous the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-i- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-i- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sanders W.E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE; 92340571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse)
                                                                                                                                                                                                                                                      EMBL; M87861;
EMBL; M72332;
                                                                                                                                                                                                                                                                                                                                                              use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEM3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQKIIYK 210
                                                                                                                                                                                        INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Molecular cloning and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 EHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQKTTTK 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: CA(2+) DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      THE CELL SURFACE
                                                                                                                                                                                                                                                                                                                                                                                                                                                THE HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                        MGI:98280; SELP.
                                                                                                                                                                                                                                        A42755; A42755.
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loning and analysis of in vivo expression of murine
                                                                                                                                                                                                                                                      AAA40008.1; -.
AAA37712.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1;

PROSITE; PS50041; C_TYPE_LECTIN_2;

PRINTS; PR00343; SELECTIN.

PF00059; lectin_c; 1. PF00084; sushi; 8. PF00008; EGF; 1.

INTERPRO;

[NTERPRO; INTERPRO;

Cell adhesion;

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Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                      1 EDCNELPPRRNTEILTGSWSDQ-----TYPEGTQAIYKCRPG--YRSLGNVIMVCR 49
            FGY--NSSCTFLCAEGFVLKGNDAIQCADSGQWTAPAPFCEALQCPEFPVPS
                                                                                                                                                                   SCAEGYELDGPGEL---QCLASGIWTNNPPKCDAVQCQSLEAPPHGTM--ACMHPIAAFA
                                                IIYKENERFQYKCNMGYEYSERGDAVCTESG-W-RPLPSCEEKSCDNPYIPN
                                                                                                              TCNEGYQL--LGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH
                                                                                         YDSSCKFECQPGYRARGSNTLHCTGSGQWSEPLPTCEAIACEPPEIPIHGSMDCVPSTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83098 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                17.4%; Score 260.5; DB 1; 26.0%; Pred. No. 5.9e-14;
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N-LINKED (GLCNAC...) (PO)
N-LINKED (GLCNAC...) (PO)
N-LINKED (GLCNAC...) (PO)
PALMITATE (BY SIMILARITY).
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SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 6.
SUSHI 6.
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SUSHI 8.
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A -> E (IN REF. 2).
E5173074D2F66E68 CRC64;
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REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF-like domain; Lectin;
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(POTENTIAL).
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            393
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PROSITE; PS01186, EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Weller A., Isenmann S., Vestweber D.;

"Cloning of the mouse endothelial selectins. Expression of both E and P-selectin is inducible by tumor necrosis factor alpha.";

J. Biol. Chem. 267:15176-15183(1992).

-i- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
      DOMAIN
                                                                   CHAIN
                                                                                                                                                                                                                                                                   PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q00690;
01-APR-1993
01-APR-1993
                                            DOMAIN
                                                                                    SIGNAL
                                                                                                     Selectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                          PFAM;
                                                                                                                                                                                                                                                                                                       INTERPRO; IPRO00561; -.
INTERPRO; IPRO01304; -.
INTERPRO; IPRO02396; -.
                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M80778; AAA37547.1; EMBL; M87862; AAA37577.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                             HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Murine endothelial leukocyte-adhesion molecule 1 is a clos
structural and functional homologue of the human protein.";
Eur. J. Blochem. 206:401-411(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN
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                                                                                                                                                                                                                                                                                      ; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                       MGI:98278; SELE.
                                                                                                                                                                                                                                           PF00059; lectin_c; 1. PF00084; sushi; 6.
                                                                                                                                                                                                                                                                                                                                                                                                             P16581;
                                                                                                                                                                                                                          PR00343; SELECTIN.
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92340571.
                                                                                                     Signal;
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Eutheria;
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                                                                                                     Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Huijsduijnen R.H., Losberger C., Whelan
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
                                                             BY SIMILARITY.
E-SELECTIN.
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Sciurognathi;
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Best Local Similarity 27.9
Matches 69; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             SYPMNTTCTFDCVEGYRRYGAQNLQCTSSGIWD--NETPSCKAVTCDAIPQPQNGFVSCS
                                                                                                                                            CDNPYIP 255
                                                                                                                                                                                                             DVING-----SPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-W-RPLPSCEEKS
                                                                                                                                                                                                                                                                                      -KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS-P
                                                                                                                                                                                                                                                                                                                                                                                 GGNVEEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENG- 137
                                                                                                 CPSLDVP
                                                                                                                                                                                                                                                                MKCLPSASGP---FQNGSSCEFSCEEGFELKGSRRLQCGPRGEWDSKKPTCSAVKCDDVP
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                       2000,
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EGF-LIKE.
6 X SUSHI (SCR) REPEATS.
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SUSHI 2.
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SUSHI 5.
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BY SIMILARITY.
BY SIM
                       16:49:21
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Title:
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Listing first 45 summaries
                                                                                                                                                                                                                                                 Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
SPTREMBL_14:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebi:
6: sp_mammaal:*
7: sp_mhc:*
8: sp_organeli(
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebi:
14: sp_unclass
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Gapop 10.0 , Gapext 0.5
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1497
1 EDCNELPPRRNTEILTGSWS.....EKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        November 21, 2000, 16:48:48; Search time 70.54 Seconds (without alignments) 350.782 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                           297973 seqs, 93374136 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
: sp_phage:*
): sp_plant:*
l: sp_rodent:*
2: sp_virus:*
3: sp_vertebrate:*
4: sp_unclassified:*
                                                                                                                                                                                        sp_archea:*
sp_bacteria:*
sp_fungi:*
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sp_invertebrate:*
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                                                                                                                                            sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	5	4	ω	N	_	Result No.
289.5	289.5	290.5	290.5	290.5	293	298.5	298.5	298.5	301	308.5	310	320	322.5	322.5	332.5	440	699	1497	Score
19.3	19.3	19.4	19.4	19.4	19.6	19.9	19.9	19.9	20.1	20.6	20.7	21.4	21.5	21.5	22.2	29.4	46.7	100.0	Query Match
559	497	2014	661	315	363	2489	2039	559	679	522	259	645	550	550	360	1053	669	449	Query Match Length
11	11	6	6	σ	σ	4	4	4	11	σ	12	12	12	12	12	13	Φ	4	DB
Q63135	Q63612	Q29530	Q29531	Q28770	002839	Q16744	Q16745	Q9UQV2	Q99254	Q28769	P87616	Q9WRU2	040912	P88903	80LA60	Q91275	Q28085	Q14570	ij
Q63135 rattus norv	Q63612 rattus norv	Q29530 pan troglod	Q29531 pan troglod	Q28770 papio hamad	002839 sus scrofa	Q16744 homo sapien	Q16745 homo sapien	Q9uqv2 homo sapien	Q99254 mus musculu	Q28769 papio hamad	P87616 cowpox viru	Q9wru2 macaca mula	O40912 kaposi's sa	P88903 kaposi's sa	Q9ytq8 ateline her	Q91275 paralabrax	Q28085 bos taurus	Q14570 homo sapien	Description

22 C C C C C C C C C C C C C C C C C C	20 21 22 23 25 25 26
274.5 272 271 270.5 270.5 267.5 268.7 268.7 266.7 266.5 267.2 255.5 255.5	287 284.5 284.5 283.5 280.5 279 277.5 277.5
18.2 18.2 18.2 18.1 18.1 18.1 17.9 17.8 17.8 17.8 17.8 17.5 17.2 17.2 17.2	19.0 19.0 19.0 18.9 18.5 18.5
285 285 417 369 369 483 1652 274 285 285 285 347 533 579 357 452 1032	1911 263 263 263 263 263 1124 560 522
66 66 67 67 67 67 67 67 67 67 67 67 67 6	6 5 5 12 12 6
019127 019127 019127 035520 979138 979138 0264735 9991519 9991519 019121 028982 978361 978361 008569 060736 013866 013866 013866 013866 013866 013866 013866	Q29528 Q89859 Q07/033 Q89076 Q89076 Q89061 Q89061 Q892328 Q22328 Q22328 Q22328
7 60 5 5	Q29528 papio hamad Q89859 variola vir Q87033 variola vir Q89076 variola vir Q89076 variola vir Q89071 variola vir Q9vyr4 drosophila Q23328 caenorhabdi Q28797 pan troglod

ALIGNMENTS

F F	E :	7 5	7 5	DR.	DR	DR	DR	DR	RL	RA	RP	RN	RL	RA	RP	RN	RL	RT	RT	RΑ	RX	RP	RN	RL	RT	RΑ	RX	RΡ	RN	8	8	SO	GN	DE	ΡŢ	ΔŢ	Ŋ	AC	B	014570	RESULT
SIGNAL 1 18 POTENTIAL.		\neg	PRO: IPRO	P10998:	Z29665;	U56979;	EMBL; M12383; AAA52013.1;	•	Thesis (1993), Inmunologia, Hospital Trias I Pujol, Spain.		SEQUENCE OF 1-9 FROM N.A.		Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.		SEQUENCE OF 1-19 FROM N.A.	[3]	J. Immunol. 136:3407-3411(1986).	and the Ba f	mplement protein H: homology with	en T., Wetsel R.A., Tack B.F.;	861	SEQUENCE OF 226-449 FROM N.A.	[2]	Biochem. J. 249:593-602(1988).	cid sequence of	J., Day A.J., Harris T.J.R., Sim R.B.;		SEQUENCE FROM N.A.		Primates;		Homo sapiens (Human).	HF OR CFH.	COMPLEMENT FACTOR H PRECURSOR.	13,	(TrEMBLrel. 01,	\vdash	**	Q14570 PRELIMINARY; PRT; 449 AA.	70	LT 1

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                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                          MEDLINE; 96202005.

Soames C.J., Day A.J., Sim R.B.;
Soames C.J., Day A.J., Sim R.B.;
"Prediction from sequence comparisons of residues of factor in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).

EMBL; X98697; CAA67257.1; -.

HSSP; P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                            028085;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGM
                                                                                                                                                                                                                      INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 11.
                                                                                                                                                                                                                                                                                                                       TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
123 VILNGQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIP 182
                                                                                                                                                                                                                                                                                                                                                      Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28085
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                         196
                                                                     136
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                        76 GTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEYVKCLPVTAPE 135
                                                                                                                                             Local Similarity
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                    DVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP 255
                                         NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                        NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP 195
                                                                                      GSPHLAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LPSCEEKSCDNPYIPNGDYSPLRIK 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                        669
669 AA;
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449 AA;
                                                                                                                                   Conservative
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75683 MW;
                                                                                                                                       46.7%;
63.4%;
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51033 MW;
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                                                                                                                                   26;
                                                                                                                                          Score 699; DB 6; Length 669; Pred. No. 8.2e-57;
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                                                                                                                                                                                     D0D9DB30EE747AC2 CRC64;
                                                                                                                                  Mismatches
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                                                                                                                                                                                                                         Q9YTQ8 PRELIMINARY; PRT; 360 AA.
Q9YTQ8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
Ateline herpesvirus 3.
STRAIN=73;
                                        SEQUENCE FROM N.A.
                                                                                                                                   Gammanerpesvirinae; Rhadinovirus
                                                                                                                                                                                 Viruses; dsDNA viruses, no RNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement-regulatory plasma protein from barred sand bass (Parablax neblifer)."; n
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Dahmen A., Kaidoh T., Zipfel P.F., Gigli I.;

"Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paralabrax nebulifer (barred sand bass).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GG----PEEATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN
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Pred. No. 1.6e-32;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 4
                                                                                                                                                                                                                                                                                                                      Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Maddalena Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P.S.; "Nucleotide sequence of the Kaposi sarcoma-associated herpesvirus (HHV8).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpesvirus (KSHV) (Human Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
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                                                                                                                                                         genes by KSHV.";
Science 274:1739-1744(1996).
EMBL; U75698; AAC57082.1; -.
HSSP; P10998; 1VVC.
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                                                                                                             INTERPRO; IPRO00436; -. PFAM; PF00084; sushi; 4 SEQUENCE 550 AA; 606
                                                                                                                                                                                                                                                         MEDLINE;
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                                                                                                                                                                                                                         Moore P.S., Bashoff C., Weiss R.A., Commolecular mimicry of human cytokine
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 93:14862-14867(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 189 KQCSETGRWVPDEETKCEFKVCKIPQVANGHVEVRKT--SNNVQYQYVNIKCDKGFRLQG 246
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                                Local Similarity
nes 72; Conserv
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 33 KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -ECQKRRCSTPADLLNGWYTVT-GNLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRV 133
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                                                                                                                                                                                                                                                            97094384
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360 AA; 40208 MW; 118CF83C034352A0 CRC64;
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                                 Conservative
                                                                                                               60687 MW; D4B8B2B4BACD1CB5 CRC64;
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                                21.5%; Score 322.5; DB 31.2%; Pred. No. 6e-22; tive 31; Mismatches 1
                                                                                                                                                                                                                                            Weiss R.A., Chang Y.;
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Pred. No. 4.:
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01-JAN-1998
01-MAY-2000
                                     Q9WRUZ;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 14,
01-JUN-2000 (TrEMBLrel. 14,
COMPLEMENT BINDING PROTEIN.
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HSSP; P10998; LVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neipel F., Albrecht J.C., Fleckenstein B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated rhadinovirus human herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187-4192(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaposi's sarcoma-associated herpesvirus (KSHV) (Human
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORF 04
           Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage;
                                                                                                                  Q9WRU2
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Gammaherpesvirinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-----HRPKIKNGDF
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                                                                                                                                                                                                                                                                                 EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI 203
                                                                                                                                                                                                                                                                                                                 ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-----HRPKIENGDF
                                                                                                                                                                                                                                                                                                                                                                        RCRSGYTTYARNITATCLQGGTW--SEPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
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                                                                                                                                                                                                                                                        KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI
                                                                                                                                                                                                                                                                                                                                           VKAVYTCNEGYQLLGEINYREC-----DTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM 144
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31.2%;
 Rhadinovirus
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Last annotation updat
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              Herpesviridae;
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Best Local
proteins.";
Virology 243:432-460(1998).
EMBL; X94355; CAA64102.1; -.
EMBL; Y11842; CAA72567.1; -.
HSSP; P10998; 1VVC.
                                                                Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gutorov V.V., Kotwal G.J., "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                     Safronov P.F., Petrov N.A., Riazankina O.I., Totm
Shchelkunov S.N., Sandakhchiev L.S.;
"Genes of a circle of hosts for the cowpox virus.
Dokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                               MEDLINE; 98229462.
                                                                                                                                                                STRAIN-GRI-90,
                                                                                                                                                                           SEQUENCE FROM N.A.
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J. Virol. 73:3040-3053(1999).
EMBL; AF088501; AAD21332.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searles R.P., Bergquam E.P., Axthelm_M.K., Wong S.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVCTESGW-RPLPSC------EEKSCDNPYIPNGDYSPLRI 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVNWDSNEPVCEIQKCIKPPAVEHGDYL-----PNQDVYNYGDAITFKCSLSYTLVGSTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYGVKAVYTCNEGYQLLGEINYREC---DTD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHCSDDGFWSKEKPKCVEISCKSPDVING-SPISQKIIYKENERFQYKCNMGYEYSERGD 230
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PF00084; sushi; :
NCE 645 AA; 71:
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AA; 71526 MW;
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                                                                                                                                                                                                                                                                                                                                     no RNA stage;
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Pred. No. 1.2e-21;
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Best Local :
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Q28769;
01-NOV-1996 (TrEMBLrel. 01, Creat
01-NOV-1996 (TrEMBLrel. 01, Last
01-MAY-2000 (TrEMBLrel. 13, Last
COMPLEMENT RECEPTOR (FRAGMENT)).
                                                                                                                                                                                                                                                                                                                                                                           Birmingham D.J., Logar C.M., Submitted (MAY-1990) to the EMBL; L77977; AAA99004.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                   PFAM; PF00084; sushi; NON_TER 1
                                                                                                                                                                                                                                                                                                                                             HSSP; P086U3; THE TINTERPRO; IPRO00436; -. INTERPRO; IPRO0041; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Papio.
                      168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 4. SEQUENCE 259 AA; 28193 MW;
                                                     159
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GDEEMHCS--DD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNM
                                                                                                                                                                       CNAPEQLPFARPTNLTDAS----EFPVGTYLKYECLPGYHGKPFSIICLKNSVWTSAKD- 102
                                                                                                                                                                                                    CN---ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                WDNETPICEIIPCGLPPTI-ANGDFISTS----REYFPYGSVVTYRCNLGSGRKKLFELV
                                                                             WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSG-----YKIE
                                                                                                          -KCTRKSCRNPKDPVNGMVHVI--KDIQFGSQINYSCNKGYRLIGS-SSATCIISGNTVI 158
                                                                                                                                        {\tt RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SG-WRP-LPSC 244
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                                                                                                                                                                                                                                           84;
                                                                                                                                                                                                                                                                                                                   522 AA; 56626 MW;
                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                    20.6%; Score 308.5; DB 6; 29.8%; Pred. No. 1.1e-20;
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Pred. No. 3.4e-21;
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                                                                                                                                                                                                                                                                                                                 312FCBE03ADF19DC CRC64;
                                                                                                                                                                                                                                      Mismatches 111;
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J. EXP. Med. 181:151-159(1995).
EMBL; U17128; AAA78271.1; -...
EMBL; U17123; AAA78271.1; JOINED.
EMBL; U17124; AAA78271.1; JOINED.
EMBL; U17125; AAA78271.1; JOINED.
EMBL; U17126; AAA78271.1; JOINED.
EMBL; U17127; AAA78271.1; JOINED.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 (CR2) (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kim Y.U., Kinoshita T., Molina H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21-367 FROM N.A. MEDLINE; 95105691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 90229754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mechanisms of both human decay-accelerating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Holers V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGD; MGI:88489; Cr2.
INTERPRO; IPRO00436; -.
PFAM; PF00084; Sushi; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         222 GYEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPNGDYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GEPSIYCTSKDDQVGIWSGPAPQCIIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQP 273
  205
                                                          209
                                                                                                              185
                                                                                                                                                                        152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GFVMKGPRHVQCQALNKWEPELPSCSRVCQPPPEILHGEHTP 315
                                                                                                                                                                                                                       ENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCSDD-----GFWSKEK 184
                                                                                                                                                                                                                                                                                 HINTG--IEFGSTITYSCNQGYRLIGD-SSATCIVSDNTVMWDNDMPLCESIPCESPPAI 151
                                                                                                                                                                                                                                                                                                                                  TLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDGWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                            SDKSEFAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                              SDQT-YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTF 78
                                                          PQCIPRVKCPMPEIENGLVESGFKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPP
                                                                                                                                                                        SNGDFYSSSRD---SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPP 208
                                                                                                              PKCV-EISCKSPDVING----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M36470; AAA37449.1;
P10998; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
  -QKIIY----KENERF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74916 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20.1%;
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JOINED.
JOINED.
JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 301; DB 11;
Pred. No. 7.6e-20;
1; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52FC00FDCED20CDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hourcade D., Seya T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crry/p65 uses the erating factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               679
     -QYKCNMGYEYSERGDAVCTESG-W-RPL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specific
membrane
                                                                                                                 SPIS----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus
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Qy
RESULT
Q16745
ID Q1
AC Q1
DT 01
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Best Local
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Q9UQV2;
01-MAY-2000
Q16745;
Q16745;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hourcade D., Miesner D.R., Atkinson J.P., Holers V.M.; "Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit a prediction of a secreted form of complement receptor type 1."; J. Exp. Med. 168:1255-1270(1988).

EMBL: X14362; CAA32541.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HUMAN CRI MRNA FOR C3B/C4B RECEPTOR SECRETED FORM PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; [1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269
                                                                                           305
                                                                                                                    253
                                                                                                                                              245
                                                                                                                                                                         223
                                                                                                                                                                                                    185
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                                                                                                                                                                                                                                                         129
                                                                                                                                                                                                                                                                                  116
                                                                                                                                                                                                                                                                                                             73
                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                               18 CNAPEWLPFARPTNLT----DEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD- 72
                                                   12
                                                                                                                                                                                                                                                                                                                                                                                          3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTCEVKSCD--AIPN 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPTCFMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPGYTLIGTNLVECTSLGTWSNTV 328
                                                                                                                                                                                                                                                                                                                                     RKCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                            YDLRGAASMRCTPQGDWSP 323
                                                                                                                    Y----IPNGDYSP 261
                                                                                                                                              FVMKGPRRVKCQALNKWEPELPSCSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCEPG
                                                                                                                                                                        YEYSERGDAVCTE-SGWRP-LPSCEE-----
                                                                                                                                                                                                    EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPG
                                                                                                                                                                                                                              DEEMHC - - SDD - - GFWSKEKPKC - VEISCKSPDVINGSPIS - QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                         WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                                                                                                                                                  WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                            -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89010527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000834; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sushi; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                    19.9%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                      49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 298.5; DE Pred. No. 1e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DBFFE965CA179D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                             2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                      111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                             ----KSCDNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo
                                                                                                                                                                                                                                                                                                                                                                                                                       73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unit and
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                     168
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(TrEMBLrel. 01,

Created)

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Matches
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                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                         EMBL: L17401
EMBL: L17402
EMBL: L17403
EMBL: L17405
EMBL: L17405
EMBL: L17406
EMBL: L17407
EMBL: L174109
EMBL: L17411
EMBL: L17411
EMBL: L17411
EMBL: L17412
EMBL: L17413
EMBL: L17413
EMBL: L17414
EMBL: L17414
EMBL: L17417
EMBL: L17420
EMBL: L17421
                                                                                                                                                                                                                            PFAM; PF00084; sushi; 30.

PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_2.

SEQUENCE 2039 AA; 223603 MW; B82FCB11C6B16635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
EMBL;
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EMBL;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vik D.F., Wong W.W.;
"Structure of the gene for the F allele cand sequence of the coding region unique
J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TremBLrel.
01-MAY-2000 (TremBLrel.
COMPLEMENT RECEPTOR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                             INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 94065175.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vik D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                          98
                                                          60
                                                                                       43
                                                                                                                                                                     Local
                                                                                                                     w
                                                                                                   -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 153
                                                   RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                  CNAPEWLPFARPTNLT----DEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L17395;
L17396;
L17397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L17398;
L17399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L17391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L17418; AAB60694.1;
                                                                                                                                                     86; Conserv
                                                                                                                                                                                                                                                                                             IPR000834; -.
IPR001424; -.
                                                                                                                                                                                                                                                                                                                          IPR000436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong W.W.;
(JUN-1993)
                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                      AAB60694 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; AAB60694.1;
; AAB60694.1;
; AAB60694.1;
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AAB60694.1;
AAB60694.1;
AAB60694.1;
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AAB60694.1;
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AAB60694.1;
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AAB60694.1;
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AAB60694.1;
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Pred. No. 5e-1
19; Mismatches
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5e-19;
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                                                                                                                                              Gaps
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Q16744
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Q16744;
Q1670V-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
COMPLEMENT RECEPTOR 1.
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EMBL; L17418: AATTCA
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EMBL;
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"Structure of the gene for the F allele of complement receptor type 1 and sequence of the coding region unique to the S allele.";
J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 13, Last annotation update)
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Primates;
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JOINED
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                                                                                        Int. Immunol.
EMBL; D70897;
HSSP; P10998;
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INTERPRO; IPR001424; -.
PFAM; PF00084; Sushi; 37.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
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                                                                                                                                                                                                                                                                                                                          Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
PORCINE MEMBRANE COFACTOR PROTEIN.
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INTERPRO; IPRO00436; -.
                                                                                                                                                                              Toyomura K., Fujimura T., Murakami H., Inoue N., Takeda J., Kinoshita T.; "Molecular cloning of a pig homologue of the control of the pig homologue of the control of the pig homologue of the control of the control of the pig homologue of the control of the cont
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                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE; 97343414.
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SEQUENCE
                                            PFAM; PF00084; sushi; 4.
                                                                                                                                                             (CD46)."
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117426; AAB60695.1;
117427; AAB60695.1;
117428; AAB60695.1;
117429; AAB60695.1;
117429; AAB60695.1;
117430; AAB60695.1;
117430; AAB60695.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEEMHC -- SDD -- GFWSKEKPKC - VEISCKSPDVINGSPIS - QKIIYKENERFQYKCNMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RKCQKRPCGHPGDTPTGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
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86; Conser
                                                                       IPR000436; -
  363
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                          BAA20476.1;
1VVC.
                                                                                                                                         9:869-876(1997).
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -IPNGDYSP 261
  39692
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Pred. No. 6.3e-19;
  8A5FF329B8E03153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
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  CRC64;
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                                                                                                                                                                                                                                                                                                                                 Euteleostomi;
Sus.
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Query Match

19

Score

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Length 363;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                Matches
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Q28770;
Q1-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                        Birmingham D.J., Logar C.M., Shen X.P., Chen V Submitted (MAY-1996) to the EMBL/GenBank/DDBJ EMBL; L77978; AAA99005.1; -. HSSP, P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Cre 01-NOV-1996 (TrEMBLrel. 01, Las 01-NAY-2000 (TrEMBLrel. 13, Las COMPLEMENT RECEPTOR (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-BONE MARROW;
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228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMAWSEPSPLCEKILCKPPGEIPNGKYTNSHKD---VFEYNEVVTYSCLSSTGPDEFSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI---MVCR-KGEWVALNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRK-CQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLG-EINYRECDTDG- 115
GFVMKGPRRVQCQALNKWEPELPSC-SRVCQPPPDVLHGERTQRDKDIFQTGQEVFYICE 286
                                                                                                                                   WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREY-HFGQAVRFVCNSG------YKIE 167
                                                                                                                                                                                                        RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG---- 115
                                                                                                                                                                                                                                    CNAPEQLPFARPTELI ---- DESEFSIGTHLKYECRPGYYGRPFSIICLKNSVWTSAKD-
                                                                                                                                                                                                                                                                CN---ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSERGDAVC-TESGWRP-LPSC--EEKSCDNPYIPN----GDYSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GESSLFCIGKDEWSSDPPECKVVKCPYPVVPNGEIVSGFGSKFYYKAEVVF--KCNAGFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPIS---QKIIYKENERFQYKCNMGYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---WINDIPICEVYKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG----YKIE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQEACRRKACSNLPDPLNGQVSYPNGDML-FGSKAQFTCNTGFYIIGAETVY--CQVSGN 155
                           GYEYSERGDAVCTE-SGWRP-LPSCEEKSCDNP-----
                                                         GEPSIYCTSNEDQVGIWSGPAPQCIIPNKCTPPNVENGILVSVNRSLFSLNEVVEFRCQP
                                                                                    GDEEMHCSDD----GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNM
                                                                                                                   WDNETPICEKISCGLPPTI-DNGDFFSA----NKEYFHYGSVVTYRCNLGSGGRKLFELV
                                                                                                                                                                           -RCIRKSCRNPRDPVNGMVHVI--KDIQFGSQINYSCTEGHRLIGS-SSATCIISGNTVI 112
                                                                                                                                                                                                                                                                                                                                                                     315 AA;
                                                                                                                                                                                                                                                                                                                                                                                     315
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                                                                                                                                                                                                                                                                                                                                                                     35172 MW;
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                                                                                                                                                                                                                                                                                             19.4%; Score 290.5; DB 6
26.5%; Pred. No. 2.8e-19;
Live 52; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47;
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                     305B314AE752824F CRC64;
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                                                                                                                                                                                                                                                                                                107;
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Search completed: November 21, 2000, 16:48:51 Job time: 329 sec

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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
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Misting first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
                    // SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1990.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1992.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1993.DAT:
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// SIDS1/gcgdata/geneseq/geneseqp/AA1998.DAT:
// SIDS1/gcgdata/geneseq/geneseqp/AA1999.DAT:
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7SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
7SIDS1/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/geneseq/geneseqp/AA1987.DAT:*
/SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*
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141.789 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	DB	ID	Description
_	721	62.0	240	18	W39154	Human partial Comp
2	627	53.9	216	18	W39155	Clone pRRB9FH410 C
ω	261	22.4	299	17	W06881	Decay accelerating
4	261	22.4	376	20	Y50035	Human complement r
ъ	261	22.4	381	8	P70048	Human decay accele
o	261	22.4	381	10	P94773	Decay accelerating
7	261	22.4	381	16	R66683	
8	261	22.4	381	18	W26317	-
9	261	22.4	381	20	Y31740	Human CD55 and 791
10	261	22.4	381	20	W73505	Decay accelerating
11	261	22.4	440	8	P70049	Human decay accele
12	261	22.4	440	10	P94774	Membrane bound dec

44444	337	33333 432 5432	26 27 28 29 30	20 21 22 23 24 25	13 14 15 16 17
252 252 252 252	254 253.5 253.5	2 2 2 2 2 2 5 5 5 5 5 5 5 5	2 2 2 2 2 2 3 2 3 5 5 5 5 1 5 5 5 5 5	2222222 555555555555555555555555555555	261 261 261 261 261 259 257.5
$\mu\mu\mu\mu\mu\mu$				21.9 21.9 21.9 21.9 21.9 21.9	22.4 22.4 22.4 22.3
555555555555555555555555555555555555555	543 484 543	778 1930 2039 2039 2317	5543 543 543	543 543	440 440 543 577 543 496
13 13 13				13315	16 18 13 17 17 13
R28558 R28563 R28549 R28551 R28551	R28545 R28548 W99892 Y81934	89 81 75 21	R28568 R28569 R28570 R28571	R47154 R47155 R47155 R28550 R28553 R28565 R28566	R66684 W27483 R28557 W06882 W28547 Y55752
4 (109N, 4 (117P) 4 (64K, 4 (65T) 4 (116K)	CRI-4 (3/Y) analog CRI-4 (57V, 59K) a CRI-4 (57V, 59K) a Porcine E-selectin Porcine E-selectin CRI-4 (92T) analog	Human comple Human comple Human comple Human C3b/C4 CR1 protein.	CR1-4 (318- CR1-4 (347T CR1-4 (366- CR1-4 (266- CR1-4 (364- Amino	ence of solence of solence of solence of sole 4 (64K) and 4 (85R, 87N 4 (121Q) and 4 (318R, 31	Decay accelerating Human glycophospha CR1-4 (99H, 103E) Membrane co-factor CR1-4 (52S, 53S, 5 Human CR1 protein CR1-4 (14S) analo

ALIGNMENTS

RESULT W39154

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AC NAME OF A CONTROL OF A CONTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-MAR-1997;
09-APR-1996;
09-APR-1996;
06-MAR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W39154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W39154 standard; Protein; 240 AA.
Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human partial Complement factor H protein fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1998 (first entry)
                                                                                                                                           WPI; 1997-512742/47.
N-PSDB; V02790.
                                                                                                                                                                                                                                                                                  Enfield DL, Hass GM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                         (BARD-) BARD DIAGNOSTIC SCI INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97US-0812481.
96US-0015083.
96US-0630048.
97US-0038614.
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                                                                                                                                                                                                                                                                                            Kinders RJ;
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Best Local
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This partial protein is found in clone pRRB9FH410 and represents
                                       Example 6B; Fig 6B; 104pp; English.
                                                                             H related antigen, or nucleic acid encoding
                                                                                           Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Fact
                                                                                                                                                             N-PSDB; V02791.
                                                                                                                                                                           WPI; 1997-512742/47.
                                                                                                                                                                                                                   Enfield DL,
                                                                                                                                                                                                                                                                                                               09-APR-1996;
09-APR-1996;
                                                                                                                                                                                                                                                                                                                                                   06-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                         09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone pRRB9FH410 CFH related protein fragment.
                                                                                                                                                                                                                                                     (BARD-) BARD DIAGNOSTIC SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9738136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         urogenital cancer; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               such proteins and a CFH antigens can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This partial protein sequence represents a region of the human tumour-associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens isolated from clone prbB99FH410 (see W39155). The detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           H related antigen, or nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6B; Fig 6B;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 INGSPISQKI 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 AA;
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                                                                                                                                                                                                                   Hass GM,
                                                                                                                                                                                                                                                                                         96US-0015083.
96US-0630048.
97US-0038614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62.0%; Score 721; DB 18; Length 240; 100.0%; Pred. No. 1.2e-59;
                                                                                                                                                                                                                 Kinders RJ;
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                                                                                             complement Factor
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Best Local :
                                                                                           A portion (W06881) of the complement-inhibitor, decay accelerating factor (DAF), is used in novel chimeric proteins of formula A-R1-B-R2-C, where A and C are peptides (W06875-79, W06883-90) able to bind glycosaminoglycans (esp. heparin) present on cell surfaces, R1 is a portion of DAF or membrane co-factor protein (McP, see also W06880), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may have complement inhibitor activity. The chimeric
                                                   W06880), R2 is DAF when R1 is MCP or MCP when R1 is DAF, and B is a peptide that may have complement inhibitor activity. The chimeric proteins (see also W06882) are directed to cell surfaces where they inhibit complement-mediated coll justs. They are used to treat and
                    sepsis, adult respiratory distress syndrome, reperfusion injury and
                                           prevent disease states in which complement plays a role,
                                                                                                                                                                                                                                           Disclosure; Page 25; 33pp; English.
                                                                                                                                                                                                                                                                                                      comprise membrane
                                                                                                                                                                                                                                                                                                                    Chimeric proteins for inhibiting complement-mediated cell lysis
                                                                                                                                                                                                                                                                                                                                                                                              Creasey AA, Innis MA,
                                                                                                                                                                                                                                                                                     peptide sequences
                                                                                                                                                                                                                                                                                                                                                          WPI; 1996-506167/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement inhibitor; membrane co-factor protein; MCP; decay accelerating factor; DAF; chimeric protien; glycosaminoglycan; heparin; cell lysis; sepsis; adult respiratory distress syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-NOV-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decay accelerating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W06881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W06881 standard; Protein; 299 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement factor H related protein with homology to a region of the human tumour associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 reperfusion injury; cell damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAR-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      155 AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISOKI 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             216 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0435149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96WO-US06301.
                                                                                                                                                                                                                                                                                                  co-factor protein and decay accelerating
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99.1%;
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Pred. No. 6e-51;
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                                             e.g.
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                                                                                                         (decay accelerating factor). Complement regulatory proteins (CRPs) such as DAF and CD59 are membrane bound proteins that protect an organism's cells from attack by its own complement. Hyperacute rejection of a xenotransplant occurs because natural antibodies in the human recipient bind to the endothelium of the donor organ and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement regulatory protein; decay accelerating factor; DAF; immune reaction; xenotransplantation; xenograft; transplant, organ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human complement regulatory protein DAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y50035 standard; Protein; 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune reaction; xenotransplantation; xenograft; tran-
rejection; hyperacute; inhibition; protection; heart;
                                                                                                                                                                                                                                              Claim 18; Fig 15; 88pp; English
                                                                                                                                                                                                                                                                                  e.g. preventing xenotransplant rejection in humans
                                                                                                                                                                                                                                                                                                      use of cells or tissues expressing complement regulatory molecules for,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   kidney; pancreas; thyroid; islet cell; neurons; stem cell; tissue;
resistant to attack by human complement, thus preventing organ rejection. Methods of causing donor animal cells to hyperexpress CRPs
                                   activate complement, thereby initiating rapid rejection. Hyperexpression of this protein in pig cells may be useful for the protection of xenotransplanted organs, as greatly increased amounts of functional CRP molecules will be expressed. The organ should be
                                                                                                                                                                                                         This sequence represents human complement regulatory protein DAF
                                                                                                                                                                                                                                                                                                                                            WPI; 1999-620420/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                Rushmere NK, Hinchliffe SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        98GB-0007520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-GB01085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 17; Length 299;
                                                                                                                                                                                                                                                                                                                                                                                  Van
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                                                                                                                                                                                                                                                                                                                                                                                    Den Berg CW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lung; liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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P70048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωy
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used for protection of xenotransplants. For example, organs, tissue and cells can be generated which are resistant to complement attack and hence to hyperacute rejection when transplanted into humans. The methods can be used for organs, such as heart, lung, liver, kidney, pancreas and thyroid; cells, such as islet cells, neurons, and stem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cells; or tissues, such as skin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P70048 standard; protein; 381 AA.
                           The probable phosphatidylinositol derivatisation site is Cys(330). The DAF variant is useful for treating paraoxysmal nocturnal haemoglobinuria, or inflammatory or cell lytic autoimmune diseases. It may be used to ameliorate allograft rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P70048;
                                                                                                                                                                                     WPI; 1987-308481/44.
N-PSDB; N70047.
                                                                                                                                                                                                                                   Caras
                                                                                                                                                                                                                                                                                               02-MAY-1986;
                                                                                                                                                                                                                                                                                                                            01-MAY-1987;
                                                                                                                                                                                                                                                                                                                                                                                         EP244267-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decay acceleration factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human decay acceleration factor variant #1.
                                                                                                                                     New decay accelerating factor variants - using recombinant DNA procedures.
                                                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                          04-NOV-1987
                                                                                                          Disclosure; Page 15-17; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             54 VALNPLRKCOKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                    W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                 86US-0859107
                                                                                                                                                                                                                                                                                                                            87EP-0303944
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                        /label=putative transmembrane region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22.4%; Score 261; DB 20; 29.9%; Pred. No. 1.3e-16; tive 42; Mismatches 84;
                                                                                                                                                         obtained with the factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                           γď
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or autoimmune diseases. See also N70046, N70048.

SQ

Sequence

381 AA;

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RESULT
P94773
ID P9
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P9
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DT 04
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DT 06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š
                                                                                                          Matches
                                                                                                                                      Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                        Recombinant DAF's are useful in treatment of inflamatory or cell lytic autoimmune diseases and allograft rejection. Useful in diagnostic compositions or in affinity purification.
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion polypeptide for targeting protein to cell membrane comprisesphospholipid anchor domain with heterologous
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; ; 61pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1989-061177/08.
N-PSDB; N91043.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (GETH ) GENETECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO8901041-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune disease; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DAF; allograft rejection; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Decay accelerating factor (DAF) of clones lambda 33 and lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P94773 standard; protein; 381 AA.
                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         207 sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
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1 EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54 VALNPLRKCOKRPCCHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYOLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
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                                                                                                                                                                                                                                                    381 AA;
                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87US-0083757.
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                                                                                                                             22.4%; Score 261;
29.9%; Pred. No. 1
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                                                                                           s; Score 261; DB 10;
s; Pred. No. 1.4e-16;
42; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42; Mismatches
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                                                                                                                                                  Length 381;
                                                                                              Indels
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                                                                                        Gaps
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                                                                                        12;
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                    A probe (given in Q79865) based on the N-terminal sequence of human decay accelerating factor (DAF) was used to screen a HeLa cell lambda cDNA library. Isolated clones encoding membrane-bound DAF (mDAF) were obtained, and the full sequence of mDAF cDNA was determined (Q79863). The GPI signal domain of mDAF may be fused to a heterologous protein and targeted to cell membrane surfaces.
                                                                                                                                                                                                                                                                                                                                              02-MAY-1986;
06-AUG-1987;
19-DEC-1991;
12-FEB-1993;
                                                                                                                                                                     Liposome(s) for targetting particular cells contg. fusion protein of glyco:phosphatidyl:inositol anchor and heterologous targetting protein, e.g. for delivering toxins to infected or
 Sequence
                                                                                                                                   Disclosure; Fig.
                                                                                                                                                                cancer cells.
                                                                                                                                                                                                                                          N-PSDB; Q79863
                                                                                                                                                                                                                                                                                    Caras IW;
                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5374548-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Decay accelerating factor; DAF; mDAF; fusion protein; liposome; cell targeting; glycophosphatidylinositol; GPI; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R66683;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R66683 standard; Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               262 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 DEEMHC----SDDGFWSKEKPKC------VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54
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                                                                                                                                                                                                                                                     1995-035649/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                           86US-0859107.
87US-0083757.
91US-0811048.
93US-0017934.
                                                                                                                                                                                                                                                                                                                                                                                                                    86US-0859107
                                                                                                                              la-1f; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "probable phosphatidylinositol
    derivatization site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity Matches 70; Conserv
This protein sequence comprises human decay accelerating factor (DAF), a protein that has C3 complement inhibitor activity. Claimed retroviral vector particles express a complement inhibitor such as DAF, and are thereby protected from inactivation upon exposure to body fluids containing complement. Also claimed are: (1) a producer cell producing the vector particle; and (2) a chimeric retroviral envelope protein (see also W26326) with at least part of the N-terminal receptor-binding domain removed and replaced by a protein domain having a complement inhibitor activity. The vector is used in a claimed method for transducing cells in the presence of a body fluid containing complement, preferably ex vivo, especially for gene therapy, e.g. of hereditary or acquired blood disorders by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 retrovirus; vector; gene therapy; stem cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAF; decay accelerating factor; human; C3 complement inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human decay accelerating factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W26317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W26317 standard; Protein; 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5643770-A
                                                                                                                                                                                                                      Disclosure; Column 41-46; 32pp; English.
                                                                                                                                                                                                                                                                        Retroviral vector particle expressing complement inhibitor activity
                                                                                                                                                                                                                                                                                                     N-PSDB; T84471
                                                                                                                                                                                                                                                                                                                                                                                      (ALEX-) ALEXION PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       21-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                        WPI; 1997-350243/32.
                                                                                                                                                                                                                                                                                                                                                     Mason JM, Squinto SP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                        tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DG----WINDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
                                                                                                                                                                                                                                                       transducing cells in body fluids containing complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                      94US-0278630
                                                                                                                                                                                                                                                                                                                                                                                                                                                       94US-0278630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Sig_peptide 35..381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 1.4e-16;
2; Mismatches 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transduction of haematopoietic stem cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
The present sequence represents a new human tumour associated antigen, 791Tgp72, which is over-expressed on a wide range of solld tumours. The amino acid sequence of 791Tgp72 is identical to that of human CD55, although the glycosylation patterns of the 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Y31740 standard; Protein; 381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   osteosarcoma; vaccine; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human CD55 and 791Tgp72 tumour associated antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-NOV-1999 (first entry)
                                                                                                                Cancer vaccine containing CD55 family polypeptide, to induce at least one of T helper, cytotoxic T cell or natural killer immune
                                                                                                                                                                                                                                                            26-FEB-1998;
                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                 02-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                     Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   791Tgp72; colorectal cancer; breast cancer; ovary cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CD55; decay accelerating factor; DAF; tumour associated antigen;
                                                                      Claim 4; Fig 10; P 82pp; English.
                                                                                                                                                         N-PSDB; X87914, X87915.
                                                                                                                                                                           WPI; 1999-540585/45
                                                                                                                                                                                                    Durrant LG,
                                                                                                                                                                                                                                                                                                                                             WO9943800-A1
                                                                                                                                                                                                                                                                                                                                                                                                               Peptide
                                                                                                    response
                                                                                                                                                                                                                              (CANC-) CANCER RES CAMPAIGN TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 ehsiyctvnndegewsgpppecrgksltskvpptvgkpttvnvpttevsptsgk 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ဖ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                    Spendlove
                                                                                                                                                                                                                                                            98GB-0004065
                                                                                                                                                                                                                                                                                        99WO-GB00582
                                                                                                                                                                                                                                                                                                                                                                                     /note= "signal peptide"
35..380
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.4%;
                                                                                                                                                                                                                                                                                                                                                                         "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 261; DB 18;
Pred. No. 1.4e-16;
2; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            261
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RESULT 10
W73505
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C (see X87914 and X87915) which are identical over the entire coding
C region, but differ in the 5' and 3' non-coding regions. A claimed
C cancer vaccine comprises a polypeptide of the CD55 family, including
C full-length CD55 or 791Tgp72, or an antigen, polypeptide, fragment
C or derivative of CD55 or 791Tgp72. Claimed cancer vaccines also
C include nucleic acids encoding CD55 or 791Tgp72 actigen
C include nucleic acids encoding CD55 or 791Tgp72 antigen
C cancer patient involve administering the cancer vaccine. A method
C of isolating 791Tgp72 antigen from cells expressing the antigen
C is also claimed. The cancer vaccines induce at least one of T
C helper, cytotoxic T cell or natural killer immune responses,
C possibly also production of neutralizing antibodies and complement-
C mediated lysis. They are useful for treating e.g. colorectal,
C preast or ovarian cancer or osteosarcoma, where these are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Example 3; Page 8-9; 15pp; Japanese
                                                                 Vector having complement controlling factor - useful for gene
                                                                                                                                  N-PSDB; V08935
                                                                                                                                                       WPI; 1999-074147/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DAF; decay accelerating factor; human; compliment protein; gene therapy;
                                                                                                                                                                                                   (DINA-) DINABEKKU KENKYUSHO KK
                                                                                                                                                                                                                                                          15-MAY-1997;
                                                                                                                                                                                                                                                                                                      15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                        02-DEC-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Decay accelerating factor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W73505 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            associated with overexpression of 791Tgp72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              262 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR----SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                          97JP-0125965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   381 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261
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Qy Ъ οy Ъ Оy Qy

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RESULT 11
P70049
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The protein sequence is a variant of decay acceleration factor, sDAF. DAF and variants are useful for treating paraoxysmal nocturnal haemoglobinuria, or inflammatory or cell lytic autoimmune diseases. They may be used to ameliorate allograft rejection or autoimmune
                                                                            Disclosure; Page 18-20;
                                                                                                       using recombinant DNA procedures.
                                                                                                                     New decay accelerating factor variants -
                                                                                                                                                                 WPI; 1987-308481/44.
                                                                                                                                                      N-PSDB; N70048.
                                                                                                                                                                                                                              (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                            02-MAY-1986;
                                                                                                                                                                                                                                                                                        01-MAY-1987;
                                                                                                                                                                                                                                                                                                                      04-NOV-1987
                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decay acceleration factor; sDAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human decay acceleration factor variant #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P70049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P70049 standard; protein; 440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human decay accelerating factor (DAF) protein. DAF can be used in the viral vector of the invention. The viral vector contains a factor controlling the function of a human complement protein, particularly a membrane combining type protein. The viral vector, which is stable in situ, is useful for gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          262 ehsiyctvnndegewsgpppecrgksltskvpptvgkpttvnvpttevsptsgk 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYOLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92 efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                            86US-0859107
                                                                                                                                                                                                                                                                                      87EP-0303944.
                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 35..440
                                                                                                                                                                                                                                                                                                                                                                              /label= DAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.4%;
                                                                         20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 261; DB 20;
Pred. No. 1.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                       obtained with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 381;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                     factor
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P94774
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Best Local Similarity
Best Local Similarity Matches 70; Conserv
                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      See also N70046 and N70047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P94774;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P94774 standard; protein; 440
                                                                                                                                                                            Fusion polypeptide for targeting protein to cell membrane comprisesphospholipid anchor domain with heterologous
                                                                                                                                                                                                                                                                                                           06-AUG-1987;
                                                                                                                                                                                                                                                                                                                                    03-AUG-1988;
                                                                                                                                                                                                                                                                                                                                                             09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                     WO8901041-A.
                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAF; allograft rejection; affinity purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Membrane bound decay accelerating factor (sDAF).
                                                                                      Recombinant DAF's are useful in treatment of inflamatory or cell lytic autoimmune diseases and allograft rejection. Useful in diagnostic compositions or in affinity purification.
                                                                                                                                                                                                                    N-PSDB; N91044.
                                                                                                                                          Disclosure; ; 61pp; English.
                                                                                                                                                                                                                                WPI; 1989-061177/08
                                                                                                                                                                                                                                                                                 (GETH ) GENETECH INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     262 ehsiyctvnndegewsgpppecrgksltskvpptvqkpttvnvpttevsptsqk 315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sgssvqwsdplpecreiyc----pappqidngiiqgerdhygyrqsvtyacnkgftmig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
 Conservative
                                                                                                                                                                                                                                                                                                                                    88WO-US02648
                                                                                                                                                                                                                                                                                                           87US-0083757
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             22.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches 84;
  42;
 Score 261; DB 10;
Pred. No. 1.6e-16;
2; Mismatches 84;
    84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 440;
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                          Length 440;
    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          02-MAY-1986;
06-AUG-1987;
19-DEC-1991;
12-FEB-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R66684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R66684 standard; Protein; 440
                                                                                                                                                                                Liposome(s) for targetting particular cells contg. fusion protein - of glyco:phosphatidyl:inositol anchor and heterologous targetting protein, e.g. for delivering toxins to infected or cancer cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Decay accelerating factor; DAF; sDAF; fusion protein; liposome; cell targeting; glycophosphatidylinositol; GPI; drug delivery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Decay accelerating factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-JUL-1995
                                                                           A probe (given in Q79865) based on the N-terminal sequence of human decay accelerating factor (DAF) was used to screen a HeLa cell lambda cDNA library. Isolated clones encoding soluble DAF (sDAF) were obtained; the full sequence of sDAF cDNA is given in Q79864 and the deduced protein sequence in R66684.
                                                                                                                                                                                                                                                                                         Caras IW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             US5374548-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                    Sequence
                                                                                                                                                        Disclosure; Fig. 2a-2g; 36pp; English.
                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                WPI; 1995-035649/05
                                                                                                                                                                                                                                                                                                                (GETH ) GENENTECH INC
                                                                                                                                                                                                                                                                                                                                                                                                           02-MAY-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20-DEC-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                  Q79864.
                                                     440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                          86US-0859107.
87US-0083757.
91US-0811048.
93US-0017934.
                                                                                                                                                                                                                                                                                                                                                                                                            86US-0859107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
  22.4%;
    Score
Pred.
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  261; DB 16;
No. 1.6e-16;
               Length 440;
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The present sequence is human glycophosphatidylinositol (GPI) anchored DAF. GPI anchored DAF was used in the development of a novel surface bound to a homologous complement restriction factor (HCRF), where the surface is not a surface to which HCRF binds in vivo. The surface can be used in medical apparatus (e.g. extra-corporal circulation systems, tubing, valves, membranes, pumps, oxygenators, catheters, cannulas, fluid reservoirs or prostheses), medical dressings, surgical equipment, diagnostic kits (e.g. kits for determining whether a patient has an abnormality
                                                                                                                                                                                                                                                                                                                                         31-OCT-1996;
22-MAR-1996;
28-MAR-1996;
                                                                                                                                                                                 Surfaces which prevent or reduce complement activation - having surface bound homologous complement restriction factor \,
                                                                                                                                                        Example 1; Fig 1; 50pp; English.
                                                                                                                                                                                                                                                WPI; 1997-489571/45
                                                                                                                                                                                                                                                                                                          (IMUT-) IMUTRAN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                   12-MAR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09735886-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; glycophosphatidylinositol; GPI; anchored DAF; surface; homologous complement restriction factor; HCRF; medical apparatus; medical dressing; surgical equipment; diagnostic kit; prevention; purification device; reduction; complement activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human glycophosphatidylinositol anchored DAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W27483 standard; Protein; 440 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
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96GB-0006073.
96GB-0006516.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= sig_peptide
35..440
/label= mat_peptide
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WPI; 1992-375009/46
                                             Atkinson JP,
                                                                                                                                                   03-MAY-1991;
                                                                                           (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                   28-APR-1992;
                                                                                                                                                                                                                                                                                                         EP512733-A.
                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                      11-NOV-1992.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      short consensus repeat; regulator of complement C3b binding; C4b binding; human complement type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CR1-4 (99H, 103E) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R28557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28557 standard; peptide; 543 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          which prevents the complement system from working normally or from being properly regulated) and purification devices (e.g. for purifying complement components). The surface can be used to reduce or prevent activation of complement, and to reduce morbidity due to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEMHC---SDDGFWSKEKPKC------VEISCKSPDVIN-----GSPISQK 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   efcnrscevptrlnsaslkqpyitqnyfpvgtvveyecrpgyrrepslspkltclqnlkw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --stavefckkkscpnpgeirngqidvpggilf--gatisfscntgyklfgsts-sfcli 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                             Hourcade D,
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                                                                                                                                                   91US-0695514
                                                                                                                                                                                                   92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                 /note= "Ser substituted by His (SCR-9)" 103
                                                                                                                                                                                                                                                                                                                                                                                                                                       99
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511..543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               510
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                                          Krych M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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1 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection, for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
169 epsiyctsnddqvgiwsgpapqciipnkctppnvengilvs 209
                              169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS 204 : ::| :|| | | | | | | :| : | | | :| | | :|
                                                                                             113 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
                                                                                                                                                116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                          57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligh-ssaeciisgdtvi 112
                                                                                                                                                                                                                      3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                        2 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels 32; Gaps
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Search completed: November 21, 2000, 16:43:42 Job time: 281 sec

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Gapop 10.0 , Gapext 0.5
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 LEM2_PIG
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VAF_CAVPO
VCP_VACCV
C4BP_HUMAN
MCP_HUMAN
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DAF1_HOUSE
LEM2_HUMAN
C4BP_MOUSE
LEM3_HUMAN
LEM2_RAT
             LEM2_CANFA
LEM2_MOUSE
C4BP_RAT
C4BP_SOVIN
LEM3_SHEEP
CR2_MOUSE
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Q01102 mus musculu
P16109 homo sapien
P98105 rattus norv
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EMBL; Y00716; CAA68704.1; -.

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EMBL; M65294; AAA35948.1; -.

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PDB; 1HFH; 15-JUL-93.
PDB; 1HFI; 15-JUL-93.
MIM; 134370; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. MOI. BIOI. 232:268-284(1993).

-: FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PATHWAY.

-! SIMILARITY: CONYAINS 20 SUSHI (SCR) REPEATS.

-! CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
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Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.;

"Solution structure of the fifth repeat of factor H: a second example of the complement control protein module.";

Biochemistry 31:3626-3634(1992).
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STRUCTURE
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Eukaryota; Metazoa;
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Mammalia; Eutheria; Rodentia;
                                                                                   EMBL;
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                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Moriwaki K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Munoz-Canoves P., Tack B.F., Vik D.P.;
"Analysis of complement factor H mRNA expression: dexamethasone IFN-gamma increase the level of H in L cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 90148935.
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, M31979; AAA37762.1;
A26154; NBMSH.
                , p08603; 1HFI.
MGI:88385; CFH.
RPRO; IPR000436;
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PRO; IPR000436; -. PF00084; sushi; 20
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"Glycophospholipid membrane anchor attachment. Molecular analysis the cleavage/attachment site.";
J. Biol. Chem. 266:1250-1257(1991).
          J. Biol. Chem.
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01-AUG-1988 (Rel. 08, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation updat
COMPLEMENT DECAY-ACCELERATING FACTOR PRECUR
                                                     Moran P., Raab H.,
                                                                   MEDLINE; 91093238.
                                                                                    GPI-ANCHOR.
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                                                                                                                                            "Isolation of two forms
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Metazoa; Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cloning of decay-accelerating factor suggests novel use of splicing
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                                                  Kohr W.J.,
                                                                                                                                Ishikawa Y., Choi N.-H., Tobe T., Tomita M.;
ms of decay-accelerating factor (DAF) from human
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                                                                                                          1074:326-330(1991)
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-!- SUBCELLULAR (HANCA FORM):
-!- AUTHOR FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE.
-!- TISSUE SPECIFICITY: EXPRESSED ON THE PLASMA MEMBRANES OF ALL CELL TYPES THAT ARE IN INTIMATE CONTACT WITH PLASMA COMPLEMENT PROTEINS: IT IS ALSO FOUND ON THE SURFACES OF EPITHELIAL CELLS LINING EXTRACLLULAR COMPARMENTS. AND VARIANTS OF THE MOLECULE ARE PRESENT IN BODY FLUIDS AND IN EXTRACELIDIAR MATRIX.
-!- DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE ACTIVE SITE ON SCR3 (BY SIMILARITY).
-!- POLYMORPHISM: DAF IS RESPONSIBLE FOR THE CROMER BLOOD GROUP SYSTEM. IT CONSISTS OF AT LEAST SEVEN HIGH-TICIDENCE (CR(A), TC(A), DR(A), ES(A), WES(B), UMC, AND ITC) AND LOW-INCIDENCE (TC(B), TC(C), AND WES(A)) ANTIGENS THAT RESIDE ON DAF. IN THE EXPRESSION OF DAF, RESPECTIVELY. IN THE CASE OF THE DR(A-) PHENOTYPE. A SINGLE NUCLEOTIDE SUBSTITUTION WITHIN EXON 5 ACCOUNTS FOR TWO CHANGES: A SIMPLE AMINO ACID SUBSTITUTION SPLICING EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THE BASIS OF THE ANTIGENIC VARIATION, AND AN ALTERNATIVE SPLICING EVENT THAT UNDERLIES THE DECREASED EXPRESSION OF DAF IN THIS PHENOTYPE.
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THE RECEPTOR FOR ECHOVIRUS 7 AND RELATED VARUESES (ECHOVIRUSES 13, 21, 29 AND 33).

SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT HOMODIMER (MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lublin D.M., Mallinson G., Poole J., Reid M.E., Thompson E.S. Ferdman B.R., Telen M.J., Anstee D.J., Tanner M.J.A.; "Molecular basis of reduced or absent expression of decay-accelerating factor in Cromer blood group phenotypes."; Blood 84:1276-1282(1994).
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Almond J.W.;
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DISULFIDE BONDS IN SUSHI DOMAINS.
                                                                                                                            SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
                                 DATABASE: NAME=PROW; NOTE=CD guide CD55 entry;
WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD55.HTM".
                                                                                                (RCA) FAMILY
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EMBL; M31516; AAA52169.1; -.

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EMBL; M45799; AAA52170.1; -
EMBL; M64653; AAA52170.1; J
EMBL; M64356; AAA52170.1; J
EMBL; S72858; AAC66633.1; -
PIR; BA5359; B26359.
PIR; A26359; A26359.
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262
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                                                                      207
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EHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQK 315
                                                                                                                                                                            VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                  EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   group
                                DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                          --STAVEFCKKKSCPNPGEIRNGQIDVPGGILF--GATISFSCNTGYKLFGSTS-SFCLI
                                                                                                                                                                                                                EFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKW
                                                                      SGSSVQWSDPLPECREIYC----PAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIG
                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                      -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG
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                                                                                                                                                                                                                                                                                                       22.4%;
29.9%;
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                                                                                                                                                                                                                                                                                                                                                                               M₩;
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REMOVED IN MATURE FORM.
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SER/THR-RICH.
                                                                                                                                                                                                                                                                                        42;
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nchor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                               /FTId=VAR_001997.

R -> P (IN TC(C) ANTIGEN).
/FTId=VAR_001998.

L -> R (IN WES(A) ANTIGEN).
/FTId=VAR_001999.

S -> L (IN DR(A-) ANTIGEN).
/FTId=VAR_002000.

A -> P (IN CR(A-) ANTIGEN).
/FTId=VAR_002001.
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Pred.
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GPI-ANCHOR.

HTCFTLTGLLGTLVTMGLLT -> SRPVTQAGMRWCDRSSL
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                                                                                                                                                                                                                                                                                                                                                                               -> I (IN REF. 1).
-> M (IN REF. 2).
29138EEB6B4B565E CRC64;
                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                         261; DB 1;
No. 6.5e-16;
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Sushi; Polymorphi
                                                                                                                                                                                                                                                                                                                            Length 381;
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PIR; PIR;

EMBL;

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RESULT 4
CR1_HUMAN
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P17927;
01-NOV-1990
01-NOV-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-or send an email to licenseage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WONG W.W., Klickstein L.B., Smith J.A., Weis J.H., Fearon D.T.;
"Identification of a partial CONA clone for the human receptor for
complement fragments C3b/C4b.",
Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).
-i- FUNCTION: CRL, PRESENT ON ERYTHROCYTES, LEUKOCYTES, GLOMERULAR
PODDCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE
BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CR1 OR C3BR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Human C3b/C4b receptor (CR1). Demonstration of long homologous repeating domains that are composed of the short consensus repeatcharacteristics of C3/C4 binding proteins.";
J. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Identification of distinct C3b and C4b recognition sites in the human C3b/C4b receptor (CR1, CD35) by deletion mutagenesis."; J. Exp. Med. 168:1699-1717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANT IGEN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fearon D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Klickstein L.B., Wong W.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 503-2039 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fearon D.T.;
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                                                                                                                                                                                                                              EMBL;
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BL; M11569; AAA52297.1; -.
BL; M11617; AAA52298.1; -.
BL; M11618; AAA52299.1; -.
BL; Y00816; CAA68755.1; -.
BL; X05309; CAA28033.1; -.
BL; X05309; CAA28033.1; -.
BL; X054748; A24748.
R; A24748; A24748.
R; B24748; C24748.
R; C24748; C24748.
R; S03843; S03843.
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.

MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A

LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A

CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL

TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
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SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith J.A., Weis J.H., Wilson J
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PF00084; sushi, 30.
ement pathway; Glycoprotein; Transmembrane; Repeat; Signal;
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7 X SUSHI
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SUSHI C5.
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7 X SUSHI (SCR) REPEATS, LONG
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9; Mismatches 83
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
E-SELECTIN PRECUSSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2)
                                                                                                                                                                                                                                                                          EMBL; L39076;
EMBL; U08350;
HSSP; P16581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
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-!- FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS AND
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZED I
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVES
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matis L.A., Rother R.P.;
"Molecular and functional analysis of porcine E-selectin
potential role in xenograft rejection.";
Biochem. Biophys. Res. Commun. 204:763-771(1994).
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TISSUE-AORTIC ENDOTHELIUM;
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                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE-AORTIC ENDOTHELIUM;
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PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1
PROSITE; PS01186; EGF_2; 1
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GLYCOLIPIDS).

FUNCTION: PLAYS AN IMPORTANT ROLE IN ACUTE CELLULAR ALLOGRAFT PUNCTION.

REJECTION AND PROBABLY ALSO IN XENOGRAFT REJECTION.

SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

SIMILARITY: OOTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 4 SUBJECTION FEBREATS; PORCINE E-LECTIN LACKS

SIMILARITY: CONTAINS 4 SUBJECTION FEBREATS; PORCINE E-LECTIN LACKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                                                                           196
                                                                                                310
                                                          369 LEVPREINMSCSGEPV 384
                                                                             195
                                                                                                                  135
                                                                                                                                     251
                                                                                                                                                        78
                                                                                                                                                                                             22
                                                                                                                ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS
                                                                                                                                     VSCNHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQP
                                                                                                                                                     FTLTGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                           QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQN---GD
                                                                                                                                                                                            OTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPC---GHPGDTPFGT 77
                                                                             PDV-----INGSPI 203
                                                                                               KNG-LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSS
                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                484
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                 AA;
           STANDARD;
                                                                                                                                                                                                                                                                                    52567 MW;
                                                                                                                                                                                                                          21.8%; Score 253.5; DB 1
28.6%; Pred. No. 3.8e-15;
                                                                                                                                                                                                                  36;
                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC...) (POTEN

N-LINKED (GLCNAC...) (POTEN

N-LINKED (GLCNAC...) (POTEN

C -> Y (IN REF. 2).

L -> F (IN REF. 2).

T -> N (IN REF. 2).

K -> N (IN REF. 2).

V -> A (IN REF. 2).

V -> M (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 X SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL)
C-TYPE LECTIN (SHORT FO
                                                                                                                                                                                                                                                                 NLFLPAAPNAFNPMDPTKCLLT (I AFF74FE25C1FD013 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E-SELECTIN
             PRT;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                          GLCNAC.
GLCNAC.
GLCNAC.
             340
             B
                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SHORT FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like domain; Lectin;
                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                           (IN REF.
                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                       484;
                                                                                                                                                                                                                    21;
                                                                                                                                                                                                                                                                             2
                                                                                                                                                                                                                  Gaps
                                                                                                                                        309
                                                                                                                                                                              250
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9;

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DISULFID DISULFID
                                           CARBOHYD
                                                         CARBOHYD
                                                                                    DISULFID
                                                                                                    DISULFID
                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institute. There are no restrictions modified and this statement is not removed. Usage hy and a license arrange.
                                                                         DISULFID
                                                                                                                                                                             DOMAIN
                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-1996
01-FEB-1996
01-NOV-1997
                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                           REPEA1
                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                            Alternative splicing;
                                                                                                                                                                                                                                                                                                                                       PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                      EMBL; S67775; AAC60609.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                         INTERPRO; IPRO00436; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nickells M.W., Alvarez J.I., Lublin D.M., Atkinson J.P., "Characterization of DAF-2, a high molecular weight form of decay-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of DAF-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               accelerating factor (DAF; CD55), as a covalently cross-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAF OR CD55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunol. 152:676-685(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTM: THE SER/THR-RICH DOMAIN IS HEAVILY O-GLYCOSYLATED.
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR. ALTERNATIVE PRODUCTS: TWO FORMS OF DAF (DAF-2, SHOWN HERE, AND DAF-1) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOR FUNCTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION FOR THE ACTIVE SITE ON SCR3 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: MONOMER (MAJOR FORM) AND NON-DISULFIDE-LINKED, COVALENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERFERES WITH THEIR ABILITY TO CATALYZE THE CONVERSION OF C2 AND FACTOR B TO ENZYMATICALLY ACTIVE C2A AND BB AND THEREBY PREVENTS THE FORMATION OF C4B2A AND C3BBB, THE AMPLIFICATION CONVERTASES OF THE COMPLEMENT CASCADE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THIS PROTEIN RECOGNIZES C4B AND C3B FRAGMENTS THAT CONDENSE WITH CELL-SURFACE HYDROXYL OR AMINO GROUPS WHEN NASCENT C4B AND C3B ARE LOCALLY GENERATED DURING C4 AND C3 ACTIVATION. INTERACTION OF DAF WITH CELL-ASSOCIATED C4B AND C3B POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMODIMER (MINOR FORM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94110622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eutheria;
                                                                                                                                                                                                                                                                                                                            pathway; Plasma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 (Rel. 33, Created)
6 (Rel. 33, Last sequence update)
7 (Rel. 35, Last annotation update)
DECAY-ACCELERATING FACTOR (CD55) (FRAGMENT).
                                           <1
313
313
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<1
121
183
246
247
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184
107</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                      a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                  312
340
243
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118
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2243
315
53
104
117
117
            37180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                          4
                                                                                                                                                                                                                                                                                                            GPI-anchor;
          MW;
BY SIMILARITY.
BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-ANCHOR (BY SIMILARITY).
MW; D3D865C058204290 CRC64;
                                                                                                                                                                                                                                                                                                                    Glycoprotein; Membrane; Repeat;
                                                                                                                                                                                     COMPLEMENT DECAY-ACCELERATING FACTOR.
REMOVED IN MATURE FORM (BY SIMILARITY
4 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 2.
SUSHI 3.
SUSHI 4.
                                                                                                                                                                         SER/THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                            Sushi.
                                                                                                                                                                                                                                                             FORM (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                      for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                       no
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EMBL;

D55667; BAA09514.1; D55656; BAA09514.1; D55657; BAA09514.1; D55658; BAA09514.1; D55659; BAA09514.1; D55660; BAA09514.1;

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or send an email to license@isb-sib.ch).

license

is not removed. Usage by and for commercial agreement (See http://www.isb-sib.ch/announce/

restrictions

is in

entities requires a

use by non-profit institumodified and this statement

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _CAVPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Immunol. 155:3037-3048(1995).
-!- FUNCTION: PREVENTS THE FORMATION AND/OR ACCELERATES DISSOCIATION OF C3 CONVERTASE.
                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Multiple isoforms of guinea pig decay-accelerating factor (DAF) generated by alternative splicing.";
J. Immunol. 155:3037-3048(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HARTLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAF_CAVPO STANDARD; PRT; 507 AA.
Q60401; Q60402; Q60403; Q60404; Q60405; Q60406; P97254; P97255;
P97256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nonaka M., Miwa T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'Multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170 EEMHCS---DDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222 HSIYCTVNDDEGEWSGPPPECRGKSLTSKVPPTVQKPTTVNVPTTEVSPTSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                166 SGSSVQWSDPLPECREIYCPAPPQIDNG-IIQGKRD---HYGYRQSITYACNKGYTMIGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                111 --STAVEFCKKKSCPNPGEIRNGQIDVSNGILF--GATISFSCNTGYKLFGPTS-SLCLI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      54 VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALTERNATIVE PRODUCTS: THERE ARE AT LEAST SIX FORMS OF DAF TRANSCRIPTS (DISTRIBUTED IN FOUR CLASSES: GPI, TCL, TCS AND SEC) GENERATED BY ALTERNATIVE SPLICING. ONE GPI-ANCHORED FORM (GDAB-GPI), TWO FORMS WITH LONGER CYTOPLASMIC REGION (GDAB-TCL AND GDABC-TCL), TWO FORMS WITH SHORTER CYTOPLASMIC REGION (GDA-TCS AND GDAB-TCS) AND ONE SECRETED FORM (GDAB-SEC).

TISSUE SPECIFICITY: ALL THE ISOFORMS ARE WIDELY EXPRESSED. GPI AND TCS ARE THE MAJOR FORMS, WHEREAS SEC IS MINOR AND TCL IS ONLY TO TREED TO THE MAJOR TOWARD AND TOWARD 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EDCN----ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR----SLGNVIMVCRKGEW
                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
SIMILARITY: BELONGS TO THE RECEPTORS OF COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                                                                                                              (RCA) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRESENT IN TRACE LEVELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPI-ANCHOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFCNRSCEVPTRLNFASLKQPYITQNYFPVGTTVEYVCRPGYRRELSLSTKLTCLQNLTW 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95403978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=SPLEEN;
                                                                                                                                                                                                                                                                    ormatics Institute. There are no rest institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Okada N., Nonaka M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASS GPI: ATTACHED TO THE MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 251; DB 1; I
Pred. No. 4.3e-15;
37; Mismatches 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Okada H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 340;
                                                                                                                                                                                                                                                                                                                                EMBL
                                                                                                                                                                                                                                                                                                                                                        a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ВY
                                                                                                                                                                                                                                                                                                                                   outstation
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           CARBOHYD
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D55663;
D55664;
D556567;
D55657;
D55657;
D55657;
D55659;
D55660;
D55660;
                                                                                                                                                                   PRO; IPR000436; -. PF00084; sushi; 4.
                                                                                                                                                            pathway;
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BAA09516
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BAA09514.1;
BAA09514.1;
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BAA08397.1;
BAA08398.1;
BAA08399.1;
BAA08400.1;
BAA08401.1;
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31
451
507
283
93
158
220
283
458
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451
                                                                                                                                                          Glycoprotein; Membrane;
                                                                                                                                                Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                JOINED.
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                                             POTENTIAL.

COMPLEMENT DECAY-ACCELERATING FACTOR.

REMOVED IN MATURE FORM (BY SIMILARITY).

4 x SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 4.
SER/THR-RICH.
GPI-ANCHOR (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                Sushi
                                                                                                                                                            Repeat;
                                                                                                                                                             GPI-anchor;
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RESULT 8
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                  PACCY STANDARD.

VCP_VACCY STANDARD.

P1098;
01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
15-JUL-1998 (Rel. 36, East annotation (VCP) (SECRETORY PROTEIN COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN COMPLEMENT C3) (28 KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
VARSPLIC
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                                                                          MEDLINE; 88318974.
Kotwal G.J., Moss B.;
Vaccinia virus encodes a secretory polypeptide structurally related
to complement control proteins.";
Nature 335:176-178(1988).
                                                                                                                                                                             Vaccinia virus (strain WR), and Vaccinia virus (strain Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chorc
         MEDLINE; 89073756.

Kotwal G.J., Moss B.;

"Analysis of a large cluster of nonessential
                                                                  Nature [2]
                                                                                                                                   STRAIN-WR;
                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                  Orthopoxvirus.
vaccinia virus terminal transposition mutant.
                                            STRAIN-WR;
                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                           165
                                                                                                                                                                                                                                                                                                                                     257
                                                                                                                                                                                                                                                                                                                                                                                  201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYRS---LGNVIMVCRKG-E
                                                                                                                                                                                                                                                                                                                                                                                                                           W--STPAEFCEKKQCPNPGELVNGNINVTTDLLLGSQIF----FSCDPGYRLTGEAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EFCNRSCEVPPRLPYAILKSAYISKNYFPVDTVVEYECRPGYRKKYPIQSGKITCRDDLT 149
                                                                                                                                                                                                                                                                                                                                     VLTGKSHISCIVRDDVGEWSDPPPTC---RVKSPPVI
                                                                                                                                                                                                                                                                                                                                                  KIEGDEEMHC---SDDGFWSKEKPKCVEISCKSPDVI 198
                                                                                                                                                                                                                                                                                                                                                                               AFCMIKGNAVGWSSSLPTCIKIICPEPPQIENGRIVNE----EDTYEYRHVVTYECNKGF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       366
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                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 246.5;
Pred. No. 1.7e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOFORM
MISSING
MISSING
SEC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYKYUSFACGASNHWLADIAKEDLRRDFSNAQNISSLLQ
YLGAAQTQ -> DTCV (IN ISOFORM GDAB-SEC).
THYYKYDSFACGASNHHADIAKEDLRRDFSNAQNISSLLQ
VLGAAQTQ -> ANMHHMRTKNPMLYVIT (IN ISOFORM
GDA-TCS AND ISOFORM GDAB-TCS).
; D25BBB7749425210 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MISSING (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MISSING (IN ISOFORM GDA-TCS).
MISSING (IN ISOFORM GDA-TCS, GDAB-TCS AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDAB-SEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFORM GDAB-GPI)
                                                                                                                                                OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246.5; DB 1;
No. 1.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GDAB-SEC).
(IN ISOFORM GDAB-GPI).
(IN ISOFORM GDAB-GPI AND
                                                                                                                                                20-37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISOFORM GDAB-GPI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83;
  genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDABC-TCL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
              deleted
                                                                                                                                                                                           Copenhagen)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
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              from
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                                                                                                                                                                                                                            35)
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REPRESENTED TO THE PROPERTY OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X13166; CAA31564.1; -.
EMBL; M22812; AAA69605.1; -.
EMBL; M35027; AAA47997.1; -.
PIR; A31005; WMYZSP.
PDB; 1VVC; 03-DEC-97.
PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
                            DISULFID
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       SEQUENCE
                                                                                                                                                                                                                                                         REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complement activation.";

J. Mol. Biol. 272:253-265(1997)

-i- FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

-i- SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody dependent complement-enhanced neutralization of infectivity
and contributes to virulence ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "The complete DNA sequence of vaccinia virus."; Virology 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=COPENHAGEN;
MEDLINE; 91021027.
                                                                                                                                                                                                                                                                                                                                                                                                                       NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "NMR studies of a viral protein that mimics the regulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barlow P.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wiles A.P., Shaw G., Bright J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRUCTURE BY NMR OF 146-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 89:628-632(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Vaccinia virus complement-control protein prevents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isaacs S.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 92115714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goebel S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-COPENHAGEN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Virology 167:524-537(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENT ACTIVATION (RCA).
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
sen the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                    IPR000436; -
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                                                                                                                                                                                                                                                                                                                                                                       Sushi;
    28629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.P., Perkus M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  G.P.,
                                                                                                                                                                                                                                                                                                                                                                  3D-structure.
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                     SUSHI 2.
SUSHI 3.
SUSHI 4.
BY SIMIL
                                                                                                                                                                                                                                                                            SUSHI
                                                                                                                                                                                                                                                                                             4 X SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                     COMPLEMENT CONTROL PROTEIN.
                     Y SIMILARITY.
Y SIMILARITY
Y SIMILARITY.
E4322CC9A6EF8997 CRC64;
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    Chung L.P., Bentley D.R., Reid K.B.M.;
"Molecular cloning and characterization of the cDNA coding for C4b-binding protein, a regulatory protein of the classical pathway of the human complement system.;
Biochem. J. 230:133-141(1985).
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01-OCT-1993
01-NOV-1997
                                                                                                                      MEDLINE; 86301119.
Lintin S.J., Reid K.B.M.;
"Studies on the structure of the human C4b-binding FEBS Lett. 204:77-81(1986).
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"Derlyation of the sequence of the signal peptide in human C4b-binding protein and interspecies cross-hybridisation of CDNA sequence.";
                                                                                               SEQUENCE OF 80-597 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 "Genomic organization of the protein gene.";
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
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RA Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

RA Dahlback B., Smith C.A., Mueller-Eberhard H.J.;

RT "Visualization of human C4b-binding protein and its complexes with

RT "Visualization of human C4b-binding protein and its complexes with

RT Visualization of human C4b-binding protein and its complexes with

RT Visualization of human C4b-binding protein and its complexes with

RT Visualization of human C4b-binding protein C4b.";

RL Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

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01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX).
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               Lublin D.M., Liszewski M.K., Post T.W., Arce M.A., le Beau M.M., Rebentisch M.B., Lemons R.S., Seya T., Atkinson J.P.; "Molecular cloning and chromosomal localization of human membrane cofactor protein (MCP). Evidence for inclusion in the multigene
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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family of complement-regulatory proteins.";
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RA RUSSELL S.M., Spairow R.L., McKenzie I.F.C., purcell D.F.J.;
RR RUSSEL S.M., Spairow R.L., McKenzie I.F.C., purcell D.F.J.;
RT "Tissue-specific and allelic expression of the complement regulator RT "Tissue-specific and allelic expression of the complement regulator RT CD46 is controlled by alternative splicing.";
RL EUI. J. Immunol. 22:1513-1518(1992).

CC -i.FUNCTION: MCP IS AN IMPORTANT MEMBRANE PROTEIN FOR PROTECTING HOST CELLS FROM DAMAGE BY COMPLEMENT. MCP POSSESSES COFACTOR ACTIVITY FOR INACTIVATION OF C3B AND C4B BY SERUM FACTOR I. THIS WOULD CLOW MCP TO REGULATE THE COMPLEMENT SYSTEM AT THE LEVEL OF THE C3 CONVERTAGES. MAY BE INVOLVED IN THE FUSION OF THE SPERMATOGOA WITH THE OCCYTE DURING FERTILIZATION. MAY ACT BY PREVENTING COMPLEMENT CC CONVERTAGES. MAY BE INVOLVED IN THE FUSION OF THE SPERMATOGOA WITH CC SYNCYICOTROPHOBLAST LAVER OF PLACENTA.

CC -I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PRODUCED BY ALTERNATIVE SPILICING. THE FORM SHOWN IS THE TRANSCRIPT A. THE SUCCYICTOR PRODUCTS: AT LEAST 14 FORMS AND REPRESENTED IN CC ALTERNATIVE SPILCING. THE FORM SHOWN IS THE TRANSCRIPT A. THE CC ALTERNATIVE SPICING. THE FORM SHOWN IS THE TRANSCRIPT A. THE CC ALTERNATIVE SPICING IS THE 66 KDA ALPHA ISOFORM AND THE CC EBV BETA ISOFORM FOUND IN ALL TISSUE SECEPT SPERM CORRESPOND THE TRANSCRIPTS OF THE TRANSCRIPTS IN SOME ENGLY SUCCESSION OF THE TRANSCRIPTS IN SOME PLACENTAL THE SUCCESSION STOTHE TRANSCRIPTS I ERYTHROCYTES AND SOME BONE MARROW CELLS. EXCEPT EXON 13.

CC -I. PTM: EXTENSIVELY O-GLYCOSYLATED IN THE SER/THR-RICH DOMAIN
                         EMBL;
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a membrane cofactor protein-like genetic element.";
J. Immunol. 151:4137-4146(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Alternatively spliced RNAs encode several isoforms of CD46 (MCP), a regulator of complement activation."; Immunogenetics 33:335-344(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cervoni F., Fenichel P., Akhoundi C., Hsi B.L., Rossi B., "Characterization of a cDNA clone coding for human testis membrane cofactor protein (MCP, CDA6).", "MCP, CPA6).", "MCP, CPA6).", "MCP, CDA6)."
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y00651; CAA68675.1; -. S51940; AAB24802.1; -. M58050; AAA62833.1; -. AAA6283.1; -. AAA6283.1; -. S65879; AAD13968.1; -.
                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                               DATABASE: NAME=PROW; NOTE=CD guide CD46 entry; WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD46.HTM".
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                                                                                                                                                              non-profit institutions as long and this statement is not removed.
                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
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15-JUL-1998 (Rel. 3
Herpesvirus saimiri (strain 11).
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EMBL; X60283; CAA42822.1; -
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Albrecht J.-C., Fleckenstein
"New member of the multigene
herpesvirus sainiri.";
J. Virol. 66:3937-3940(1992).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            between
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                                                                                                                                                                                                                                                                                                                                       CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary structure of the her
J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: A MEMBRANE-BOUND FORM AND A SECRETED ARE PRODUCED BY ALTERNATIVE SPLICING OF THE SAME GENE. SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

SIMILARITY: CONTAINS 3 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboratic sen the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P10998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Repeat;
                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92333688
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83
83
146
209
328
     Conservative
                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nicholas
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40006
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                               20.3%;
33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane; Alternative splicing,
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Craxton
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17;
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IN LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED
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ton M.A., Coleman H., Fleckenstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       family of complement control proteins in
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                             Score 236; DB 1;
Pred. No. 9.6e-14;
                                                                                                                                           MISSING (IN SHORT : 6278A6C2ECD49669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUSHI
SUSHI
IHSUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPLEMENT CONTROL PROTEIN HOMOLOG. 3 X SUSHI (SCR) REPEATS.
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     Mismatches
                                                                                                                         ISOFORM).
ING (IN SHORT ISOFORM).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
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                                                       Length 360;
     Indels
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(POTENTIAL).
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     16;
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  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAFI_MOUSE STANDARD; PRT; 390 AA 061475; 061397; P97732; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation updat COMPLEMENT DECAY-ACCELERATING FACTOR, GPI-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and chromosomal localization of the mouse decay-accelerating factor genes. Duplicated genes encode glycosylphosphatidylinositol-anchored and transmembrane forms."; J. Immunol. 155:3079-3091(1995).
                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                            Fukuoka Y., Yasui A., Okada N., "Molecular cloning of murine de
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 96362213.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 7-390 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spicer A.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE; 95403982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                               immunoscreening."
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                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: BRAIN, SECRETORY EPITHELIA, SKELETAL LIVER, TESTES, THYMUS, SPLEEN AND LYMPH NODE. DOMAIN: THE FIRST SUSHI DOMAIN (SCR1) IS NOT NECESSARY FOUNTION. SCR2 AND SCR4 PROVIDE THE PROPER CONFORMATION ACTIVE SITE ON SCR3 (BY SIMILARITY).

SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: PROTECTION OF
                                                                                                                                                                                                                                                   SIMILARITY:
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY)
                                                                                                                                                                                                                                     (RCA) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAN 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSSAMEPDREYHFGQAVRFVCNSGYK--IEGDEEMHCSDDGFW-SKEKPKCVEISCKSPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --THTNVKDFYTYLDTVTYSCNDETKLTLTGPSSKLCSETGSWVPNGETKCEFIFCKLPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLY-YGSVITYTCNSGYSLIGSTTSACLLKRGGRVDWTPRPPICDIKKCKPPPQIANG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NVFEYGVKAVYTCNEGYQLLGEIN----YRECDTDGWTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seldin M.F.,
                                                                                                                                                                                                                                                                                                                                                                                                  8:379-385(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=SPLEEN;
                                                                                                                                                                                                                                                    BELONGS TO THE RECEPTORS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-TESTIS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                     CELLS FROM COMPLEMENT-MEDIATED DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                                              decay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          notation update)
FACTOR, GPI-ANCHORED PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Okada H
                                                                                                                                                                                                                                                                                                                                                                                                                               accelerating factor
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                                                                                                                                                                                                                                                                                                              IS NOT NECESSARY FOR
                                                                                                                                                                                                                                                      COMPLEMENT ACTIVATION
                                                                                                                                                                                                                                                                                                                                           SKELETAL
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Complement pathway; Glycoprotein; Membrane; Repeat; GPI-anchor;

HSSP; P08603; 1HCC. MGD; MGI:104850; DAF1.

L41366; AAB00091.1; D63679; BAA09830.1;

PFAM; PF00084; sushi; 4.

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(See http://www.isb-sib.ch/announce/

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LEM2_HUMAN
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Best Local :
                                                                                 P16581; P16111;
01-APR-1990 (Rel. 14, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID
             SEQUENCE
                                          Homo sapiens (Human)
Eukaryota; Metazoa; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                  LEM2_HUMAN
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                                                               OR ELAM1.
                                                                                                                                                                                                      TKKPTINVPSTGTP
                                                                                                                                                                                                                           CKSPDV - - - INGSP
                                                                                                                                                                                                                                                         AIYKCRPGYRSLGNVIMVCRKGEWVALNPL-----RKCQKRPCGHPGDTPFGTFTLTGG
                                                                                                                                                                                                                                             NNGIMRGESDSYTYSQVVTYSCDKGFILVGNASIYCTVSKSDVGQWSSPPPRCIEKSKVP
                                                                                                                                                                                                                                                                                      ILF--GSEINFSCNPGYRLVG-VSSTFCSVTGNTVDWDDEFPVCTEIHC----PEPPKI
                                                                                                                                                                                                                                                                                                           NVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                VEYECRPGFREQPPL----PGKATCLEDLVWSPVAQFCKKKSCPNPKDLDNGHINIPTG 179
                                                                                                                                                                                                                                                                                                                                                                         CNNGFKQVPDKSNIVVCLENGQWSSHETFCEKSCVAPERLSFASLKKEYLNMNFFPVGTI 124
                                                                                                                                                                                                                                                                                                                                                                                               CN----ELPPRRNTEIL--TGSWSDQT----
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sushi
                               Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                    305
                                Chordata;
Primates;
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285
285
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361
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25.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                    42;
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BY SIMILARITY.

A GICNAC. . . ) (POTEN OF A (IN REF. 2).
F -> A (IN REF. 2).
E -> G (IN REF. 2).
E -> G (IN REF. 2).
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Pred. No. 2.
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                               Craniata; Vo
Catarrhini;
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                                         Vertebrata; Euteleostomi;
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nes 81;
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    (LECAM2)

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-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATION PROTEIN IN POSITION 149 IS ASSOCIATION FOR THE PROPERTY DISEASE (CAD). A SIGNIFIC HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIE ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED UNSELECTED POPULATION (SER-149).
-!- SIMILARITY: TO OTHER SELECTINS/LECAMS.
-!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
-!- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
-!- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
-!- SIMILARITY: NAME-PROW; NOTE-CD guide CD62E entry;
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE; 99134508.

Ye S.O., Usher D., Virgil D., Zhang L.Q., Yochim S.E., G., Reti polymorphism detects the mutation of serine-128 CD 62E gene - a risk factor for coronary artery disease.
J. Biomed. Sci. 6:18-21(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Bu: "Insight into E-selectin/ligand interaction from the crystal structure and mutagenesis of the lec/EGF domains.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Modelling the carbohydrate recognition domain of human FEBS Lett. 319:5-11(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B.; "Endothelial leukocyte adhesion molecule 1: an inducible receptor for neutrophils related to complement regulatory proteins and lectins."; Science 243:1160-1165(1989).
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                                                                                                                                                                                                                                                                         FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZE ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIVE POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI GLYCOLIPIDS).
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Pizard R., Goelz S., McCarthy K., Ho
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PROSTTE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein;
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PFAM; PF00059; lectin_c; 1.
PFAM; PF00084; sushi; 6.
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Best Local
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"CDNA structure of murine C4b-binding protein, a regulatory component of the serum complement system.",

if the serum complement system.",

Biochemistry 26:4668-4674(1987).

11 FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3COMPUTANTS) BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

11 SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE
                                                                                                       between
the Eurc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONFLICT
SEQUENCE
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             entities
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                              s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EM European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content ified and this statement is not removed. Usage by and
                                                                                                                                                                                                                            BETA CHAIN OF C4BP.

SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
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N-LINKED (GLC
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01-APR-1993 (Rel. 25,
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P-SELECTIN PRECURSOR
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                               SELP
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mus musculus (Mouse)
                                                                                                          01-APR-1993
                                             (CD62P) (LEUKOCYTE-ENDOTHELIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                         LEM3_MOUSE
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                               OR GRMP.
                                                                                                                                                                                                                                                                                   PFPECVIVKCGPPPDISNGK--HSGTEDFYPYNHG--ISYTCDPGFRLVGSPFIGCTVVN 227
                                                                                                                                                                                                                       KTVPVWSSSPPTCEKIICSQPNILHGVIVS
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51551 MW;
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28.1%;
                                         , Last sequence update)
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(GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PADGEM)
NDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
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6 X SUSHI (SCR) REPEATS.
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SUSHI 2.
SUSHI 2.
SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 6.
BY SIMILARITY.
BY
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Pred.
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 Mammalia; [1]
                                                                                                                                                                                                                                                                                                  PROSITE;
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                             REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sanders W.E. Jr., Wilso
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J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weller A., Isenmann S., Vestweber D.;
"Cloning of the mouse endothelial selectins. E
"Cloning of the inducible by tumor necrosis
and P-selectin is inducible by tumor necrosis
J. Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                            DOMAIN
                                                                                                                                                                                                                                       Selectin;
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INTERPRO; IPRO00561; -.
INTERPRO; IPRO01304; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.

SIMILARITY: TO OTHER SELECTINS/LECAMS.

SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS

SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS TO CARBOHYDRAYES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE CELL SURFACE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMAN SUSHI-2 EQUIVALENT.
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92340571.
                                                                                                                                                                                                                                              PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
esion; Transmembrane; Glycoprotein; EGF-like domain; Lectin;
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loning and analysis of in vivo expro
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BY SIMILARITY.

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Search completed: November 21, 2000, 16:49:19 Job time: 322 sec

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Database
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1163
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16 17 18 19	6 7 8 11 11 12 13	υ + α ν + ι	Result No.
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019124	Q28797	P79138	062834	019127	019126	062838	062835	019125	035520	Q89076	Q07033	Q89859	Q89061	Q9VYR4	Q9VIU9	019128	062837	Q15429	Q29528	Q64735	Q22328	019122	Q63135	Q63612	Q9WTI9
019124 saguinus my		cerc			0			019125 saimiri sci	rattus	Q89076 variola vir	variola	variola	variola	drosophil	Q9viu9 drosophila	019128 pithecia pi	saguinus			(J)		Ol9122 callimico g	1 1		Q9wti9 cavia porce

ALIGNMENTS

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"The complete amino acid sequence of human complement factor H.";
Biochem. J. 249:593-602(1988).
Signal.
SIGNAL
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Thesis (1993), Inmunologia, Hospital Trias I Pujol, Spain.
EMBL; X07523; CAA30403.1; -.
EMBL; M12383; AAA52013.1; -.
EMBL; U56979; AAB01987.1; -.
EMBL; C2665; CAA82763.1; -.
EMBL; C29665; CA882763.1; -.
EMBL; C29665; CA882763.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-19 FROM N.A.

Vik D.P., Williams S.A.;

Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kristensen T., Wetsel R.A., Tack B.F.;
"Structural analysis of human complement protein H: homology with C4b binding protein, beta 2-glycoprotein I, and the Ba fragment of B2.";
J. Immunol. 136:3407-3411(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 226-449 FROM N.A. MEDLINE; 86169701.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENT FACTOR H PRECURSOR.
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                                                                           HSSP; PIUJJU, = INTERPRO; IPRO00436; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                     EMBL; X98697; CAA67257.1; -. HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                          Soames C.J., Day A.J., Sim R.B.;
"Prediction from sequence comparisons of residues of factor in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
                                                                                                                                                                                                                                                                                     NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=LIVER;
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                                               VILNGQAVLPK 133
                                                                                            NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                                                                                           GSPHLAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                 NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKEKPKCVEISCKSPDVINGSPISQKI 207
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669 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 449
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                           669
75683 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           449
                                                                                                                                                                                                          42.9%;
64.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51033 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                             19;
                                                                                                                                                                                                          Score 499; DB 6;
Pred. No. 1.3e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
C2AAD47F155343E3 CRC64;
                                                                                                                                                                                                                                                         D0D9DB30EE747AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1163; DB 4;
Pred. No. 4.5e-108;
                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ruminantia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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                                                                                                                                                                                                                    Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pecora;
                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 449;
                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                    H involved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                            0,
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RESULT
Q9WRU2
ID Q9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9WRU2;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q91275 PRELIMINARY; PRT; 1053 AA.
Q91275;
Q91275;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
Paralabrax nebulifer (barred sand bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopteryçi
Actinopterygii; Paralabrax.
                                                                                                     similarity to Kaposi's sarcoma-associated herpesvirus/human herpesvirus 8.";
J. Virol. 73:3040-3053(1999).
                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta rhadinovirus 17577.

Viruses; dsDNA viruses, no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last seq
01-JUN-2000 (TrEMBLrel. 14, Last ann
     SEQUENCE
                               PFAM; PF00084;
                                                                                         EMBL;
                                                                                                                                                                                      Searles R.P., Bergquam E.P., Axthelm M.K., "Sequence and genomic analysis of a Rhesus
                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE; 99174001.
                                                                                                                                                                                                                                                                                                                                      Gammaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPLEMENT BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WRU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L21703; AAA92556.1;
HSSP; P08603; 1HFH.
INTERPRO; IPR000436; -.
PFAM; PF00084; sushi; 16.
                                                            NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochem, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 neblifer).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement_regulatory plasma protein from barred sand bass (Parablax
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dahmen A., Kaidoh T., Zipfel P.F., Gigli I., "Cloning and characterization of a cDNA representing a putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE; 94318039.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 GG----PEEATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWINDIPICEVVKCLPVTAPENGKIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQCPLIHVDNNVQVI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EASYPGGRQVRVGCNVGYS--GFFKLVCVEGKWETRG--AKCQPRSCGHPGDAQFADFHL 102
                                                                                AF083501; AAD21332.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     201
                                                         IPR000436; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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     AA;
                               sushi;
  71526
                                                                                                                                                                                                                                                                                                                                      Rhadinovirus
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39.6%;
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Last annotation update)
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Pred. No. 2.4e-28;
Pred. No. 2.76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
93D8DE35ABF61EB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      645 AA
                                                                                                                                                                                                                                                                                                                                                             Herpesviridae;
                                                                                                                                                                                        macaque rhadinovirus with
                                                                                                                                                                                                                     Wong S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1053;
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RESULT
Q9YTQ8
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ID P8
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DT 01
DT 01
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Best Local
                                                                                                                                                                                                                                                                                                                                                        Matches
P88903;
01-MAY-1997
01-MAY-1997
01-MAY-2000
ORF 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Primary Structure of the Herpesvirus Ateles Genome."; Submitted (AUG-1998) to the EMBL/GenBank/DDBJ database EMBL, AF083424; AAC95530.1; -. HSSP; P10998; 1VVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ateline herpesvirus 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9YTQ8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Albrecht J.-C., Fleckenstein B.;
                                                                      P88903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO00436; -
                                                                                                                                      189
                                                                                                                                                                                            134
                                                                                                                                                                                                                      116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYGVKAVYTCNEGYQLLGEINYREC---DTD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVNWDSNEPVCEIQKCIKPPAVEHGDYL-----PNQDVYNYGDAITFKCSLSYTLVGSTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV--CRKGEWVALNP 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --GWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEGDEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NFPCDRKRCPTPADLLNGAVHIHGGDNALKFGSNISYECNEGYDLIGS-NVRFCILQDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENCK--PPHFTEYRVKSNTEKDLYSVGETAELICRPGYVTNTKIITTECLQNGTW--STP
                                                                                                                                                                MHCSDDGFW-SKEKPKCVEISCKSPDVING
                                                                                                                                                                                                                                                                         RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG--
                                                                                                                                                                                                                                                                                                    PKRNRYVSLRYVNITN--SSGSYPNGTTLQVTCRKGY--IGRQIQTVTCVNGNWTVPN--
                                                                                                                                                                                                                                                                                                                            PRRNTEI-----LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI--MVCRKGEWVALNPL 59
                                                                                                                                     KQCSETGRWVPDEETKCEFKVCKIPQVANG
                                                                                                                                                                                           NWTPRPPICEITKCKPPPTIANGTHTNI-----KEYYTYLDAVTYSCNDETKLTLTGPSS 188
                                                                                                                                                                                                                                               -ECQKRRCSTPADLLNGWYTVT-GNLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRV 133
                                                                                                                                                                                                                      -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYK--IEGDEE
                                                                                                                                                                                                                                                                                                                                                                                                                           PF00084; sushi; 4
4CE 360 AA; 4020
                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
              (TremBLrel. 03, Created)
(TremBLrel. 03, Last seq
(TremBLrel. 13, Last ann
                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                           40208 MW;
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                 Last sequence update)
Last annotation update)
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                            118CF83C034352A0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
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RESULT 040912
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QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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Best Local
                             Matches
                                                    Query Match
                                                                                                                                                                                                                                                                                                         01-JAN-1998
01-JAN-1998
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Russo J.J., Bohenzky R.A., Chien M.C., Chen J., Yan M., Parry J.P., Peruzzi D., Edelman I.S., Chang Y., Moore P. "Nucleotide sequence of the Kaposi sarcoma-associated he
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gammaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kaposi's sarcoma-associated herpesvirus (KSHV) (Human herpesvirus
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                               Neipel F., Albrecht J.C., Fleckenstein B.;
"Cell-homologous genes in the Kaposi's sarcoma-associated human herpesvirus 8: determinants of its pathogenicity?";
J. Virol. 71:4187-4192(1997).
EMBL; U93872; AAB62602.1; -.
HSSP; P1098; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFAM; PF00084; sushi; 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moore P.S., Bashoff C., Weis "Molecular mimicry of human
                                                                                                                                                                                                                                                                  Kaposi's sarcoma-associated herpesvirus (KSHV) (Human Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                               ORF
                                                                                                                                                                                                                                                                                                                                                040912;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U75698; AAC57082.1; HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                 MEDLINE; 97296220
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Gammaherpesvirinae; Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                               040912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          science 274:1739-1744(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes by KSHV."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ннув)
                                                                                             INTERPRO; IPRO00436; -.
PFAM; PF00084; sushi; 4.
SEQUENCE 550 AA; 60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                               164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
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                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-----HRPKIKNGDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VKAVYTCNEGYQLLGEINYREC-----DTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RCRSGYTTYARNITATCLQGGTW--SEPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG 89
KCRPGYRSLG-NVIMVC-RKGEWVALNPLRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYG
                                                                                                                                                                                                                                                                                                                                                                                                                               KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            550
                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 13, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60687
                                         23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U.S.A. 93:14862-14867(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cytokine
                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 270.5; DB 1
Pred. No. 6.6e-19;
                             Score 270.5; DB 12.
Pred. No. 6.6e-19;
24; Mismatches 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R.A., Chang
ytokine and c
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D4B8B2B4BACD1CB5 CRC64;
                                                                                              3A7FC1C30F79C6A6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                550
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                                                                                                                                                                                                                                                                                                                                                                A
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                                                      DB 12; Length 550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80;
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                              Indels
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>.s.;
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                               17;
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RESULT
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Best Local
                                                                                                                                 Q99254 PRELIMINARY; PRT; 679 AA.
Q99254;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 (CR2) (FRAGMENT).
                                                          Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
   Kurtz C.B.,
                   MEDLINE; 90229754
                                   STRAIN-BALB/C
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-BRAIN HIPPOCAMPUS;
Kumar V.B., Hyung C., Nakra R., Walters M., Sasser T., I
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases
EMBL; U88576; AAB48622.1; -.
HSSP; P08603; 1HCC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
DECAY-ACCELERATION FACTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PFAM; PF00084; sushi; 4. NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P78361
                                                                                                                                                                                                                                                                                                  228
                                                                                                                                                                                                                                                                                                                                                                                           114
                                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 KPDKDYYEYNDAVHFECNEGYTLVGPHSIACAVNNTWTSNMPTCELAGCKFPSVTHGYPI 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 EPDREYH-FGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                         54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52
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                                                                                                                                                                                                                                                                                          EHSIYCTVNNDEGEWSGPPPECRGKSLTSKVPPTVHKPTTVNVPTTEVSPTSQK 281
                                                                                                                                                                                                                                                                                                                       DEEMHC---SDDGFWSKEKPKC-----VEISCKSPDVIN-----GSPISQK 206
                                                                                                                                                                                                                                                                                                                                                                                   DG----WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDCN---ELPPRRNTEILTGSWSDQTY-PEGTQAIYKCRPGYR---SLGNVIMVCRKGEW 53
                                                                                                                                                                                                                                                                                                                                                        SGSSVQWSDPLPECREIYC----PAPPQIDNGIIQGERDHYGYRQSVTYACNKGFTMIG
                                                                                                                                                                                                                                                                                                                                                                                                                    --STAVEFCKKKSCPNPGEIRNGQIDVPGGILF--GATITFSCNTGYKLFGSTS-SFCLI 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                 VALNPLRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFCNRSCEVPTRLNSASLKQPYITQNYFPVGTVVEYECRPGYRREPSLSPKLTCLQNLKW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANISYVCNEGYFLVGREYVRYCMIGASGQMAWSSSPPFCEKEKC-----HRPKIENGDF 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VKAVYTCNEGYQLLGEINYREC-----DTDGWTNDIPICEVVKCLPVTAPENGKIVSSAM 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCRSGYTTYARNITATCLQGGTW--SEPTATCNKKSCPNPGEIQNGKVIFHGGQDALKYG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 AA; 37847 MW;
    O'Toole
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi;
    Christensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 261; DB 4; Pred. No. 3.3e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7B123F7F76D48962 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        347
 Weis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              85;
 J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bernardo A.;
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RESULT 10
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Best Local :
                                                                                                                                                                                                      Q28769 PRELIMINARY; PR
Q28769; 01-NOV-1996 (TrEMBLrel. 01, Crea
01-NOV-1996 (TrEMBLrel. 13, Last
01-MAY-2000 (TrEMBLrel. 13, Last
COMPLEMENT RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U17128; AAA78271.1; J
EMBL; U17123; AAA78271.1; J
EMBL; U17123; AAA78271.1; J
EMBL; U17125; AAA78271.1; J
EMBL; U17125; AAA78271.1; J
EMBL; U17126; AAA78271.1; J
EMBL; U17127; AAA78271.1; J
EMBL; U17127; AAA78271.1; J
EMBL; M36470; AAA37449.1; -
HSSP; P10998; IVVC.
MGD; MGI:88489; Cr2.
                                                    Birmingham D.J., Logar C.M., Submitted (MAY-1996) to the EMBL; L77977; AAA99004.1; -. HSSP, P08603; LHFI.
                                                                                                                                                             Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
  SEQUENCE
                PFAM; PF00084; sushi; NON_TER 1
                                                                                                            TISSUE=BONE MARROW;
                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                      Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 10. NON_TER 679 679
                                            [NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cofactor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of both human decay accelerating factor and membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kim Y.U., K
Holers V.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 21-367 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1.";
                                                                                                                                                                                                                                                                                                                                                                                                       152 SNGDFYSSSRD---SFFYGMYVTYYCHTGKNREKLFDLYGEKSIYCTSKDNQYGIWNSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE; 95105691.
                                                                                                                                                                                                                                                                                                                                                        209
                                                                                                                                                                                                                                                                                                                                                                                185 PKCV-EISCKSPDVING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SDQT-YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Exp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 144:3581-3591(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                              HINTG--IEFGSTITYSCNQGYRLIGD-SSATCIVSDNTVMWDNDMPLCESIPCESPPAI 151
                                                                                                                                                                                                                                                                                                                                                       PQCIPRVKCPMPEIENG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDGWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDKSEFAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Med. 181:151-159(1995).
                          ; IPR000436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kinoshita T., Molina H.,
 522 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
 56626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.4%;
                                                                                to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74916 MW;
                                                                                                                                                                                                                                                                                                                                                     225
                                                                                                                                                                                                                                                                                                                                                                                200
 MW;
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Last annotation updat
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                                                                                              Shen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 260; DB 11;
Pred. No. 9.5e-18;
"'Amatches 72;
                                                                                                                                                                                                                                                                                PRT;
312FCBE03ADF19DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52FC00FDCED20CDC CRC64;
                                                                                               X.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hourcade D.,
                                                                                                                                                                                                                                                                                522 AA
                                                                                                 Chen W.;
                                                                                                                                                                                                                        update)
                                                                                databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wagner L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                             Matches
                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Safronov P.F., Petrov N.A., Riazankina O.I., Totmenin Shchelkunov S.N., Sandakhchiev L.S.; "Genes of a circle of hosts for the cowpox virus."; pokl. Akad. Nauk 349:829-833(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
41KBP FRACMENT FROM LEFT END OF GENOME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cowpox virus (CPV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D17L OR C17L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41KBP FRAGMENT FROM LEFT
                                                                                                                                                                                                                                                        Proteins.";
Virology 243:432-460(1998).
EMBL; X94355; CAA64102.1; -.
EMBL; X11842; CAA72567.1; -.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                      Shchelkunov S.N., Safronov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gutorov V.V., Kotovatmenin A.V., Petrov N.A., "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-GRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Orthopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P87616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P87616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 97068532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             214 GEPSIYCTSKDDQVGIWSGPAPQCIIPNKCMPPNVENGVLVS 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 GDEEMHCS--DD--GFWSKEKPKC-VEISCKSPDVINGSPIS 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSG-----YKIE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 -KCTRKSCRNPKDPVNGMVHVI--KDIQFGSQINYSCNKGYRLIGS-SSATCIISGNTVI 158
                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE; 98229462.
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-GRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 CNAPEQLEFARETNLIDAS----EFEVGTYLKYECLEGYHGKEFSIICLKNSVWTSAKD- 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 CN---ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                              61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---W 116
                                                                  20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WDNETPICEIIPCGLPPTI-ANGDFISTS----REYFPYGSVVTYRCNLGSGRKKLFELV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG---- 115
QCIKRRCPSPRDIDNGQLDIGG---VDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVW 132
                                                                                             CNELPPRRNTEILIGSWSDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLR 60
                                                                  CCPIPSRPITMKFKGT-VDSHYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFN---
                                                                                                                                                                                                                            PF00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                              Similarity
                                                                                                                                                                                                                                            IPR000436; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                             259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                 Conservative
                                                                                                                                                                                                                              sushi;
                                                                                                                                                                                                                                                                                                                                                                                                        Safronov P.F., Totmenin A.V., Petrov N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22.0%; score 256; DB 6; Length 522; 31.1%; Pred. No. 1.7e-17;
                                                                                                                                                                                                               28193 MW;
                                                                                                                                              22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                  23; Mismatches
                                                                                                                                                Score 255.5; DB 1
Pred. No. 8.3e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                               9D1AAEF6893B859A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                   DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81; Indels
                                                                                                                                    93;
                                                                                                                                    Indels
                                                                                                                                                                 Length 259;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34;
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RESULT
Q9UQV2
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AC Q1
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Q9UQV2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit a prediction of a secreted form of complement receptor type 1.";

J. Exp. Med. 168:1255-1270(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PFAM; PF00084; sushi; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hourcade D., Miesner D.R., Atkinson J.P., Holers V.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 NPEAPICESVKCQSPPSISNGR--HNGYED--FYTDGSVVTYSCNSGYSLIGNSGVLCS- 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 INDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSD 176
                                                                                                                    Q16745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               177 DGFWSKEKPKCVEISCKSPDVING
               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
   Mammalia; [1]
                                                             COMPLEMENT RECEPTOR 1.
                                                                                                                                                                                                                                                                     129 WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                                                                             185
                                                                                                                                                                                                                                         169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS 204
                                                                                                                                                                                                                                                                                                                                73
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                                                                                                                                                                                                                                                                                                                                                                                          18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                   3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGEWS-DPPTCQIVKCPHPTISNG
                                                                                                                                                                                                                                                                                                                                                                                         CNAPEWLPFARPTNLT----DEFEEPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD- 72
                                                                                                                                                                                                                                                                                                                                                           RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                  WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG----YKIEG
                                                                                                                                                                                                                                                                                                                              -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 128
                                                                                                                                                                                                             EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVS 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X14362; CAA32541.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                559 AA;
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                                                                                                                                      PRELIMINARY;
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559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.98;
                                                                             01,
01,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        39;
                                                                           Last sequence update)
Last annotation updat
                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 255; DB 4;
Pred. No. 2.4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210
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                                                                                                                                         PRT;
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                                                                                                                                         2039 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         83;
                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                 184
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EMBL: L17406
EMBL: L17408
EMBL: L17409
EMBL: L174109
EMBL: L17411
EMBL: L17411
EMBL: L17412
EMBL: L17413
EMBL: L17413
EMBL: L17415
EMBL: L17415
EMBL: L17416
EMBL: L17417
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EMBL: L17421
EMBL: L17423
EMBL: L17423
EMBL: L17423
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INTERPRO; IPR000834; -.
INTERPRO; IPR001424; -.
INTERPRO; IPR00084; sushi; 30.
PFAM; PF00084; sushi; 30.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_2.
SEQUENCE 2039 AA; 223603 MW; B82FCB11C6B16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, 
              210
                                                                   169
                                                                                                                      154
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EMBL;
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Submitted (JUN-1993)
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"Structure of the gene for the F allele of complement receptor type and sequence of the coding region unique to the S allele.";
J. Immunol. 151:6214-6224(1993).
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                                                                                                                                                                                                                               86
                                                                                                                                                                                                                                                                               60
                                                                                                                                                                                                                                                                                                                                       43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                    3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVS 250
                                    DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS 204
                                                                                                WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                     WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                   CNAPEWLPFARPTNLT----DEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD-
                                                                                                                                                                                                        -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 153
                                                                                                                                                                                                                                                        RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117418; AAB60694.1; 117390; AAB60694.1; 117391; AAB60694.1; 117392; AAB60694.1; 117393; AAB60694.1; 117393; AAB60694.1; 117394; AAB60694.1; 117395; AAB60694.1; 117396; AAB60694.1; 117397; AAB60694.1; 117398; AAB60694.1; 117398; AAB60694.1; 117398; AAB60694.1; 117398; AAB60694.1; 117399; AAB60694.1; 117400; AAB60694.1; 117400
                                                                                                                                                                                                                                                                                                                                                                                                                                             67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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AAB60694.1;
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AAB60694.1;
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AAB60694.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 255; DB 4;
Pred. No. 1.1e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B82FCB11C6B16635 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2039;
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INTERPRO; IPH000436; -.
INTERPRO; IPH000434; -.
INTERPRO; IPH001424; -.
INTERPRO; IPH001424; -.
PFAM; PF00084; Sushi; 37.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
    SEQUENCE
                                                                  EMBL;
EMBL;
EMBL;
HSSP;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Vik D.P., Wong W.W.;
Submitted (JUN-1993)
                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vik D.P., Wong W.W.; "Structure of the gene for the F allele of complement receptor and sequence of the coding region unique to the S allele."; J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPLEMENT RECEPTOR 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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L17422;
L17423;
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L174001
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117391; AAB60695.1;
117392; AAB60695.1;
117393; AAB60695.1;
117394; AAB60695.1;
117394; AAB60695.1;
117395; AAB60695.1;
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    2489
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AAB60695.1;
AAB60695.1;
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CEE11B53F2B4FAF6 CRC64;
          UNKNOWN_3
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Best Local S
Matches 56
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                                                                                                                                                                                                                                                                                                     INTERPRO; IPRO00436; ...
INTERPRO; IPRO00561; ...
INTERPRO; IPRO01304; ...
INTERPRO; IPRO01304; ...
INTERPRO; IPRO02396; ...
PFAM; PF00008; EGF; 1.
PFAM; PF000059; lectin_c; 1.
PFAM; PF000041; sushi, 4.
PRO11TE; PS00043; SELECTIN_
PROSITE; PS00022; EGF_1; UNKNOWN_1.
PROSITE; PS00015; C_TYPE_LECTIN_1; 1.
PROSITE; PS01186; EGF_2; 1.
PROSITE; PS00041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein.
SEQUENCE 482 AA; 52341 MW; 97DC5D70B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             **Reach F.H.;

*The intron-exon structure of the porcine E-selectin-encoding gene.";

Gene 176:67-72(1996),

EMBL; U37521; AAC48680.1; -.

HSSP; P16581; 1ESL.

HSSP; P16581; 1ESL.

INTERPRO; IPRO00436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q28982 PRELIMINARY; PKT; 402 cm.
Q28982;
Q1.NOV-1996 (TrEMBLrel. 01, Created)
Q1.NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1.JUN-2000 (TrEMBLrel. 14, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Winkler H., Brostjan C., Csizmadia V., Natarajan G., Anrather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDLINE; 97075911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : ::| :|| | | | | |:| : | | |:| :| 250
310 KNG-LVKFTHSPTGEFTYKSSCAFSCEEGFELRGSAQLACTSQGQWTQEVPSCQVVQCSS
                                  135 ENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKS 194
                                                                      251 VSCNHSSIGEFAYKSTCHFTCAEGFGLQGPAQI-ECTAQGQWTQQAPVCKAVKCPAVSQP
                                                                                                                                               196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS 204 : ::| :|| | || || |:| :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86
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                                                                                                                                                                  22 QTYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVALNPLRKCQKRPC---GHPGDTPFGT 77
                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTLTGGNVFEYGVKAV--YTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAP 134
                                                                                                                                              QSLPWNTTCAFECKEGFELIGPEHLQCTSSGSWDGKKP--TCKAVTCDTVGHPQN---GD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
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                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                         52341 MW; 97DC5D70BF115944 CRC64;
                                                                                                                                                                                                                  21.8%; Score 253.5; DB 6; Length 482; 28.6%; Pred. No. 2.8e-17; tive 36; Mismatches 83; Indels 21
                                                                                                                                                                                                                    21;
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                                                                      309
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Search completed: November 21, 2000, 16:48:48 Job time: 326 sec

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Minimum
Maximum
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Perfect score:
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Maximum Match 100%
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1497
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/SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqp/AA1986.DAT:*
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Copyright (c) 1993 - 2000 Comp
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/SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:*
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181.518 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query Match	Query Match Length DB	DB	ĬĎ	Description
	1055	70.5	240	18	W39154	Human partial Comp
2	961	64.2	216	18	W39155	Clone pRRB9FH410 C
ω	303	20.2	581		R13490	Human C4 binding p
4	301.5	20.1	263		Y29859	Vaccinia complemen
ഗ	301	20.1	496	20	Y55752	Human CR1 protein
6	300.5	20.1	543		R28557	CR1-4 (99H, 103E)
7	298.5	19.9	543		R28547	CR1-4 (52S, 53S, 5
8	298.5	19.9	543	13	R28567	CR1-4 (318-321 RNP
9	298.5	19.9	778		W73147	Amino acid sequenc
10	298.5	19.9	1930	19	W45899	Human complememt r
11	298.5	19.9	2039	20	Y55751	Human C3b/C4b rece
12	298.5	19.9	2317	10	P92219	CR1 protein. Homo

Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor

Vaccinia virus SPI	Y29858	20	263	19.0	284.5	45
CR1-4 (114-117STKP	2855	13	5 4 3	٥	85	44
CR1-4 (35E, 37Y) a	2854	13	543	٥	85.	4 ω
CR1-4 (44T, 47D, 4	2854	13	543	9	86.	42
-4 (35E)	2854	13	543		86.	41
CR1-4 (92T, 94H) a	855	13	543	9	87.	40
CR1-4 (115T) analo	2856	13	543	9.	88.	39
CR1-4 (78T, 79D) a	285	13	543		88.	38
CR1-4 (116K, 117P)	2856	13	543	9.	89.	37
CR1-4 (94H) analog	2855	13	543	9.	89.	36
sequ	200	10	263		89.	3 5
Sequence of solubl	715	15	254	9.	90.	34
e of	15	15	254	9.	90.	ω
(318R,	(T)	13	543	9.	91.	32
-4 (116K	56	13	543	9.	91.	31
-4 (65T)	55	13	543	9.	91.	30
-4 (64K,	54	13	543	9.	91.	29
-4 (117P)	56	13	543	9.	92.	28
-4 (109N, 11	55	13	543	9.	92.	27
-4 (92T)	55	13	543	9.	92.	26
ein. (91	20	363	φ.	9	25
₽	41	18	363	9	o	24
57V,	54	13	543	9	93.	23
-4 (37Y)	54	13	543	9	93.	22
Ξ	81	12	2039	19.7		21
-4 (364-367	57	13	543	9	94.	20
69-376 9	856	13	543	9	94.	19
47T, 349	56	13	543	9	94.	18
21Q) anal	856	13	543	9.	94.	17
5R,	855	13	5 4 3	9	94.	16
4	855	13	543	9	94.	15
	7	13	543	9.	95.	14
14S) an	856	<u>1</u> 3	543	9.	96.	13

ALIGNMENTS

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RESULT
W39154
06-MAR-1997;
09-APR-1996;
09-APR-1996;
06-MAR-1997;
                                                                                                                                                                                                                                                                   W39154 standard; Protein; 240
                                                                                                                                                                                          urogenital cancer; medicament; modulator.
                                                                                                                                                                                                   Complement factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                   Human partial Complement factor H protein fragment 1.
                                                                                                                                                                                                                                                    W39154;
                                                                                                                                                          W09738136-A1
                                                                                                                                                                                                                                   27-APR-1998 (first entry)
                      N-PSDB; V02790.
                               WPI; 1997-512742/47.
                                               Enfield DL,
                                                               (BARD-) BARD DIAGNOSTIC SCI INC.
                                                                                                                         09-APR-1997;
                                                                                                                                          16-OCT-1997.
                                                                                                                                                                         Homo sapiens
                                                Hass GM,
                                                                                97US-0812481.
96US-0015083.
96US-0630048.
97US-0038614.
                                                                                                                          97WO-US05710
                                                Kinders RJ;
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SXCCCCCCXXXX

Length 216; Indels

Gaps

0,

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Query Match
Best Local (
                                                                                                                                                                                        06-MAR-1997;
09-APR-1996;
09-APR-1996;
06-MAR-1997;
     Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor H related antigen, or nucleic acid encoding it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This partial protein sequence represents a region of the human tumour associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens isolated from clone pRBB9FH410 (see W39155). The detection of such proteins and a CFH antigens can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                       Enfield DL,
                                                                                                                                                                                                                                                                        09-APR-1997;
                                                                                                                                                                                                                                                                                                                                     WO9738136-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone pRRB9FH410 CFH related protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W39155;
                                                                                                                                                       (BARD-) BARD DIAGNOSTIC SCI INC
                                                                                                                                                                                                                                                                                                       16-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                      Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W39155 standard; Protein; 216 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-APR-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               258 DYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 FILTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDIDGWINDIPICEVVKCLPVTAPENG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 kivssamepdreyhfgqavrfvcnsgykiegdeemhcsddgfwskekpkcveisckspdv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       related antigen, or nucleic acid encoding it
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                                                                                     1997-512742/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftltggnvfeygvkavytcnegyqllgeinyrecdtdgwtndipicevvkclpvtapeng 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 dysplrik 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDV 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ingspisqkiiykenerfqykcnmgyeysergdavctesgwrplpsceekscdnpyipng 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    cancer; medicament; modulator.
                                                                                                                                                                                                                                                                                                                                                                                                                factor H; tumour associated antigen; renal cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                      96US-0015083.
96US-0630048.
97US-0038614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1055; DB 18; Pred. No. 3.2e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                 Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
   Disulfide-bond
                                  Disulfide-bond
                                                                                                                  Region
                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           short consensus repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C4bp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of
                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R13490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R13490 standard; Protein; 581 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6B; Fig 6B; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 AVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSPDVINGSPISQKIIYKENER 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 avrfvcnsgykiegdeemhcsddgfwgkekpkcveisckspdvingspisqkiiykener
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 TCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQ 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tcnegyqllgeinyrecdtdgwtndipicevvkclpvtapengkivssamepdreyhfgq 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           monomer; complement protein; pJOD.C4bp.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C4 binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       170;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
/note= "intradomain"
65..92
                             /note= "responsible for multimer 34..80
                                                                                 524..581
                                                                                                                  465..
                                                                                                                                                 407..464
                                                                                                                                                                                 346..406
                                                                                                                                                                                                                                                  /label=
220..279
                                                                                                                                                                                                                                                                                                                                                                                /label= signal_peptide
33..581
                                                                /label= C4bp_core
                                                                                                 /label= SCR1
                                                                                                                                 /label= SCR2
                                                                                                                                                                  /label=
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                                                                                                                                                                                                                                                                               /label= SCR7
156..219
                                                                                                                                                                                                                                                                                                                               /label= SCR8
                                                                                                                                                                                                                                                                                                                                                             /label= C4bp
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                  .523
                                                                                                                                                                                                                 . 345
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                                                                                                                                                                                                                                                  279
                                                                                                                                                                                                                                 SCR5
                                                                                                                                                                                                                                                               SCR6
                                                                                                                                                                  SCR3
                                                                                                                                                                                                  SCR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Pred. No. 2.2e-73;
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W39155

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RESULT
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR the first cysteine residue bonds with the fraction. This secondary structure is responsible for the conformational flexibility of the Calp monomer. The invention covers fusion proteins in which the monomer sequence, or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) is fused to the C-terminal of a protein such as a viral receptor, cell ligand, a bacterial, viral or parasitic immunogen, enzyme, cytokine, toxin, etc. See also 013243-51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New C4 binding protein fusion proteins and DNA encoding them -
comprise assemblies of C4bp monomers linked to functional moiety,
e.g. AZT, useful as delivery vehicles in diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence was deduced from human hepatocyte (Hep G2) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-252613/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOG-) BIOGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JAN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-JAN-1990;
               16-NOV-1999
                                              ¥29859;
                                                                            Y29859 standard;
                                                                                                                                                                                                                                                                                     160
                                                                                                                                                         274
                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                        241 L-PSCEEKSCDN-PYIPNGDY 259
                                                                                                                                                                                                                                                                                                                                                                                   78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                         sppacepnscinlpdiphasw 294
                                                                                                                                                                                                                                                     PKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAV--C-TESGWRP
                                                                                                                                                                                                                                                                                                                  LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                 FTLTGGNV-----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC 128
                                                                                                                                                                                                                                                                                  kpppdirngrhsge----enfyaygfsvtyscdprfsllghasisctvenetigvwrpsp
                                                                                                                                                                                                                                                                                                                                                                                                                   tetrfktgttlkytclpgyvrshstqtltcnsdgewv-yntf--ciykrcrhpge----
                                                                                                                                                                                                                      ptcekitcrkpdvshgemvsgfgpiynykdtivfkcqkgfvl--rgssvihcdadskwnp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90US-0470888
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                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ်
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.2%; Score 303; DB 12; 30.7%; Pred. No. 1.2e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu
                                                                            263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                         273
                                                                                                                                                                                                                                                     240
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Q4 B 84

134 154

208 hptisngylssgfkrsysyndnvdfkckygyklsgsssstcspgntwkpelpkc 261

isngr--hngyed--fytdgsvvtyscnsgyslignsgvlcs-ggews-dpptcqivkcp
SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244

PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193

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 \begin{array}{l} \mathbf{X} \times \mathbf{X} \cap \mathbf{C} \cap \mathbf
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                                                                                                                                                                                                                                                                                                                                             Ϋ́
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system disorders, neurodegeneration and infections. Hyperacute rejection may also be prevented by treating the graft with SPICE before transplanting it or by using a xenograft that has been transformed to express SPICE from a gene therapy vector. SPICE is also useful as additive to blood, e.g. in an extracorporeal circulation system (coated on tubing) or in storage, also for studying complement activation. Transgenic animals that express SPICE are used as sources of xenografts. The present sequence represents a vaccinia complement control protein (VCP) encoded by the specifically claimed mutated VCP nucleotide sequence, having a silent T to A transversion at nucleotide position
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYJO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              disorders, especially hyperacute rejection, inflammation or post-
ischaemic reperfusion injury, malignancies, autoimmune diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the Vaccinia virus smallpox inhibitor of complement enzymes (SPICE) protein. SPICE is an inhibitor of complement activation, and so can be used to treat or prevent complement-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Fig 1; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New smallpox inhibitor of complement enzyme protein, used to treat complement-mediated disease, particularly hyperacute rejection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rosengard AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein; hyperacute rejection; xenograft; inflammation; post-ischaemic reperfusion injury; aultoimmune disease; immune system disorder; neurodegeneration; infection; gene therapy; blood additive; extracorporeal circulation system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-550981/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9944625-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccinia virus; smallpox inhibitor of complement enzyme; SPICE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccinia complement control protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity nes 78; Conserv
            97
                                                                                                                                                                                                                                                 40
                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                          SDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
ldigg---vdfgssityscnsgyhligesksycelgstgsmvwnpeapicesvkcqspps 153
                                                                                                                                                                                                                                    ananynigdtieylclpgyrkqkmgpiyakctgtgwtlfn---qcikrrcpsprdidngq
                                                                                                               FTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV PITTSBURGH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ahearn JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US04635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98US-0076821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%; Score 301.5; DB 20; 33.3%; Pred. No. 6.2e-18; tive 29; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                     length human CRI as expressed on erythrocytes. The CRI function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-1974;
24-FEB-1993;
01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full length human CR1 as expressed on erythrocytes. The CR1 function in vivo
                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                      and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-
CRI antibodies are used in assays, and diagnostics. The present sequence
represents the short consensus repeat (SCR) fragments of human CRI
protein long homologous repeat (LHR)-A sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 10; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiant activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A human C3B/C4B receptor (CR1) protein having antiinflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Concino MF, Wong WW, Marsh HC, Carson GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BGHM ) BRIGHAM & WOMENS HOSPITAL. (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; huma complement regulatory activity; complement pathway enzyme; tissue dama reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; long homologous repeat; LHR; SCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human CR1 protein LHR-A SCR fragment.
104 --rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtv 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYJO ) UNIV JOHNS HOPKINS (BGHM ) BRIGHAM & WOMENS HO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            short consensus repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Y55752 standard; Protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-FEB-2000
                                                                             48
                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention relates to a human C3B/C4B receptor (CR1) protein. The CR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ģ
                                                                                                       CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGE-WVALNP 58
                                   LRKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTD 114
                                                                    cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiicclknsvwtgakd 103
                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                          496 AA;
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0026134.
88US-0176532.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74US-0350238
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                                                                                                                                                                20.1%; Score 301; DB 20; 27.5%; Pred. No. 1.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makrides SC, Klickstein LB,
                                                                                                                                                 48; Mismatches 110;
                                                                                                                                                                                 DB 20;
                                                                                                                                                                               Length 496;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fearon DT,
                                                                                                                                               74;
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ip SH;
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The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of
                                                                                                             Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                              Complement activity regulator protein analogues - useful for treating auto: immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                          WPI; 1992-375009/46
                                                                                                                                                                                                                                                              Atkinson JP,
                                                                                                                                                                                                                                                                                                                                 03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Ser substituted by His (SCR-9)" Misc-difference 103 \,
                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                             EP512733-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CR1-4 (99H, 103E) analogue.
                                                                                                                                                                                                                                                                                              (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                     28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 iwdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelv 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 GWTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 PY----
                                                                                                                                                  diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYEYSERGDAVCTE-SGWRP-LPSCEE------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gfvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscep
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDEEMHC -- SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNM 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----IPNGDYSP 261
                                                                                                                                                    etc.
                                                                                                                                                                                                                                                            Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                 91US-0695514
                                                                                                                                                                                                                                                                                                                                                                     92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= SCR-2
451..510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Thr substituted by Glu (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= SCR-9
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В
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                               short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                       Misc-difference
                                                                                                                                                                                                                                                                                                                        CR1-4 (52S,
                                                                                                                                                                                                                                                                                                                                                    19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                      R28547 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
EP512733-A
                                                                                            Misc-difference
                                                                                                                                                                                     Region
                                                                 Misc-difference
                                                                                                                                                            Region
                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 WINDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligh-ssaeciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ydlrgaasmrctpqgdwspaaptcevkscdd 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     543
                                                                                                                                                                                                                                                                                                                        538,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                 /note= "Thr substituted by Ser 53
                                        54
                                                                                             52
                                                                                                                                                                                     /label= SCR-1
61..122
                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        54P) analogue.
                         /note= "Ala substituted by Pro (SCR-8)"
                                                                                                        /note=
                                                  'note= "Gly substituted by
                                                                                                                     'label=
                                                                                                                                              'label=
                                                                                                                                                                       'label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.1%;
                                                                                                                                                            .510
                                                                                                                                   543
                                                                                                          "TRUNCATED"
                                                                                                                                              SCR-8
                                                                                                                     SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 300.5; DB 13; Pred. No. 1.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -ERFQ----YKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103;
                                                  Ser
                                                                              (SCR-8)"
                                                   (SCR-8)"
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of
CR1-4 (318-321 RNPP) analogue
                                                                                                  R28567 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treating auto: immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1992-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-NOV-1992
                                  19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                             DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKEN------
                                                                                                                                                                                                                                                                                                                                                                              wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
                                                                                                                                                                                                                                                                                                                                                                                                                 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                drcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvw--sspk 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                              epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                               ydlrgaasmrctpqgdwspaaptcevkscdd
                                                                                                                                                                                                                  YEYSERGDAVCTESG-WRP-LPSCEEKSCDN 251
                                                                                                                                                                                                                                                 fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity
88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92EP-0303826
                                                                                                peptide;
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                                                                                                   543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 298.5; DB 13; Pred. No. 2.7e-17;
                                                                                                                                                                                   319
                                                                                                                                                                                                                                                                                   --ERFQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 543;
                                                                                                                                                                                                                                                                                   --YKCNMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                  -YKIEG 168
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                                                                                                                                                                                                                                                                                                                  The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are disclosed in which certain
                                                                                                                                                                                                                    positions in SCR-5-6 are substituted by amino acids from the corresponding positions in SCRs which are involved in C3b- and C4b-binding. The substitution variant given here has increased C4b-binding. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Example 8; Page 18 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant reject
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Atkinson JP, Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Asp substituted Misc-difference 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
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    57
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                                                                                                                                  Local Similarity
                                                                                         ω
                                                            N
-rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                           RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                      cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                     CNE----LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                         543 AA;
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0695514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "Phe substituted by Pro" 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "TRUNCATED"
318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= SCR-8
511..543
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= SCR-1
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                                                                                                                                 19.9%;
26.5%;
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                                                                                                                 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Krych M;
                                                                                                                                 Score 298.5; DB 13; Length 543; Pred. No. 2.7e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to suppress transplant rejection,
                                                                                                                   Mismatches
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                            an interferon-gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis,
                                                                                                                                                                              This is an amino acid sequence of the human soluble complement receptor 1 (sCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or B-cell-mediated immune response to prevent immune response-mediated
                                                                                                        expressed protein especially from cells that have been treated by gene therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                tissue rejection and destruction or clearance or inactivation of an
                                                                                                                                                                                                                                                                                   Disclosure; Fig 1; 54pp; English.
                                                                                                                                                                                                                                                                                                                                         Fragment of soluble human complement receptor 1 - useful for treating T-cell or B-cell mediated immune responses e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             dystrophin; inflammatory response; interferon-gamma secretory response; autolimmune response; neurological response; Alzheimer's disease; Parkinson's disease; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
                                                                                                                                                                                                                                                                                                                     inflammatory responses such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1998-568350/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09845430-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Annenkov A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hashimoto's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mediated immune response; inhibition; tissue rejection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; soluble complement receptor 1; sCR1; T-cell; B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the soluble complement receptor 1 (sCR1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHER/) CHERNAJOVSKY Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ANNE/) ANNENKOV A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229
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                bullosa or Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Chernajovsky Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Membrane binding element; thrombotic disease; soluble protein; complement-related disease; integral membrane protein; inflammation; short consensus repeat; SCR 1-3; CR1; complement receptor type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-links
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W45899 standard;
  Claim 22; Pages 60-61; 75pp; English
                                                                                   Derivatives of soluble poly:peptide(s) bonded to low affinity membrane binding groups - useful for treating complement-related and thrombotic diseases, providing improved localisation at cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human complememt receptor 1 (residues 1-1929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUN-1998
                                                                                                                                                                                                        WPI; 1998-110524/10
                                                                                                                                                                                                                                                          Dodd I,
                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                     08-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YEYSERGDAVCTE-SGWRP-LPSCEE------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg
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                                                                                                                                                                                                                                                          Mossakowska DEI,
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27.0%;
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                                                                                                                                                                                                                                                             Smith RAG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----KSCDNP 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents human complement receptor 1 (CR1, CD 35) N-terminal fragment. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement-related disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also to treat allergy, induce weight loss, to treat ischaemia or asthma and as immuno-modulators for treating multiple sclerosis. (A) are administered artilly to constant.
                                                                                                                                                                                                            C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            orally, topically, by injection or inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.
03-APR-1989;
                                                                                                                                                                                                                                                                                            Human C3b/C4b receptor (CR1) protein.
                                                                                                                                                                                                                                                                                                                                 22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                      06-JUN-1995;
                                                                             09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                             Y55751 standard; Protein; 2039
                                                                                                                                                       Homo sapiens
                                                                                                                                                                                              heart condition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG------YKIEG 168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watch 19.9%; Score 298.5; DB 19; Local Similarity 27.0%; Pred. No. 1.3e-16; nes 86; Conservative 49; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y-----IPNGDYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YEYSERGDAVCTE-SGWRP-LPSCEE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      epsiy cts ndd qvgiws gpapq ciipnk ctppnvengilvs dnrslfslnevve frcqpg
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                                    95US-0470652
                                                                                                                                                                                              autoimmune disorder; diagnostic
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               soluble CRI protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CRI proteins, analogues, derivatives, and anti-CRI antibodies are used in assays, and diagnostics. The present sequence represents the human CRI activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1974;
24-FEB-1993;
01-APR-1988;
 22-FEB-1990
                                                                   P92219 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full length human CRI as expressed on erythrocytes. The CRI function in vivo may be mediated through the inhibition of complement pathway enzymes. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a human C3B/C4B receptor (CR1) protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1A-P; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiant activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A human C3B/C4B receptor (CR1) protein having antiinflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; Z38150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      represents the human CR1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Concino MF,
                                                                                                                                                          330 ydlrgaasmrctpggdwsp 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AVAN-) AVANT IMMUNOTHERAPEUTICS INC.
                                                                                                                                                                                              253 Y-----IPNGDYSP 261
                                                                                                                                                                                                                            270 fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg 329
                                                                                                                                                                                                                                                                                                                                                                      154 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                            116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                  YEYSERGDAVCTE-SGWRP-LPSCEE-----
                                                                                                                                                                                                                                                                                                  epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1999-633357/54.
                                                                                                                                                                                                                                                                                                                                    DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                              -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNIV JOHNS HOPKINS.
BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carson GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2039 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wong WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74US-0350238.
93US-0026134.
88US-0176532.
                                                                   protein; 2317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19.9%; Score 298.5; 27.0%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Makrides SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20; Length 2039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fearon
                                                                                                                                                                                                                                                                  ---KSCDNP 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The CR1
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                                                                                                                                                                                                                                                                                                                                                                          209
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is full-length CR1 protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      patent). Deletion mutants, eg LHR-A for binding of C4b, and for C3b binding, be made, and LHR-B and -C can detect CR2 se
They are useful in diagnosing and treating immune disorders,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Fig 1; 191pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           perfusion injury.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of complement-related immune defects,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TCEL ) T CELL SCIENCES INC.
(UYJO ) THE JOHNS HOPKINS UNIVERSITY.
(BRIG ) THE BRIGHAM AND WOMEN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1989.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement; cofactor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR1 protein
                  253
                                                 279
                                                                                                                                           169
                                                                                                                                                                           163
                                                                                                                                                                                                          116
                                                                                                                                                                                                                                          107
                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                 3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                      wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                Y----IPNGDYSP 261
                                                                              YEYSERGDAVCTE-SGWRP-LPSCEE----
                                                                                                          epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpg
                                                                                                                                      DEEMHC -- SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                     WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                     -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 162
                                                                                                                                                                                                                                                                   RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1989-309498/42
                                           fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg
                                                                                                                                                                                                                                                                                                                                                                   86;
                                                                                                                                                                                                                                                                                                                                                                                                                                              2317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88US-0176532
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/label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                               19.9%;
                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong W,
                                                                                                                                                                                                                                                                                                                                                                               Score 298.5, DB 1
Pred. No. 1.6e-16;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carson G,
                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Concino MF,
                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                              Length 2317;
                                                                            ---KSCDNP 252
                                                                                                                                                                                                                                                                                                                                                                73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Makrides SC;
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          prevent
                                                                                                                                                                       218
                                                                                                                                                                                                     168
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В
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          20
                                        Matches
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR1-4 (114S) analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R28560 standard;
                                                                                                                                                                                                                                                                                                                                                                      Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                   specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ
                                                                                                                                                                                                                                        The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of
                                                                                                                                                                                                                                                                                                                               Claim 11; Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-375009/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-NOV-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          339 ydlrgaasmrctpqgdwsp 357
                                                                                                                                          accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                       for diagnosis etc.
                                                                                                            Sequence
                                                    Local Similarity
            3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                        87;
                                                                                                               543 AA;
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91US-0695514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Asp substituted by Ser (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= SCR-9
/note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 543 AA.
                                                    19.8%; Score 296.5; DB 13; Length 543; 26.3%; Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .510
                                                                                                                                                                                                                                                                                                                                                                                                                                               Krych M;
                                          46; Mismatches 103;
<u>:</u>
Indels 95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
 short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CR1-4 (266-274 KLKTQTNASD) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R28570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R28570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                   Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant reject
                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                              WPI; 1992-375009/46.
                                                                                                                                          Atkinson JP,
                                                                                                                                                                   (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                 03-MAY-1991;
                                                                                                                                                                                                                            28-APR-1992;
                                                                                                                                                                                                                                                      11-NOV-1992
                                                                                                                                                                                                                                                                                  EP512733-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           229 fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 wsnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988)
                            Example 8; Page 18 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289 ydlrgaasmrctpqgdwspaaptcevkscdd 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   223 YEYSERGDAVCTESG-WRP-LPSCEEKSCDN 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKEN-----
                                                      for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57 -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epsiycts ndd qvgiws gpapq ciipnkctpp nvengilvs dnrslfslnevve frcqpv\\
                                                                                                                                          Hourcade D,
                                                                                                                                                                                                 91US-0695514
                                                                                                                                                                                                                             92EP-0303826.
                                                                                                                                                                                                                                                                                                                                         266..274
                                                                                                                                                                                                                                                                                                                                                                                  /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 543 AA
                                                                                                                                                                                                                                                                                                                            /note= "ERTQRDKN substituted with KLKTQTNASD
                                                                                                                                                                                                                                                                                                                                                     /label= SCR-9
/note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                          /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                              .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----YKCNMG
                                                                                                                                                                                                                                                                                                                from SCR-8-9 to increase C3b binding"
                                                                                                                                            Krych M;
                                                                        rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                              Misc-difference
                                                                            Region
                                                                                                                                         Region
                                                                                                                                                                                                                                           C3b binding; C4b binding; human complement type 1 receptor
                                                                                                         Region
                                                                                                                                                                        Region
                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                 CR1-4 (64K) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CRl. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CRl-4 is a preferred truncated form and a number of specified substitution variants of it are disclosed in which certain positions in SCR-5-6 are substituted by amino acids from the corresponding positions in SCRs which are involved in C3b- and C4b-binding. The substitution variant given here has increased C3b-binding. The substitution variant given here has increased C3b-binding. The specification does not contain the CRl-4 sequence; amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                    short consensus
                                                                                                                                                                                                                                                                                                                                                                                             R28550 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                               19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 WINDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ydlrgaasmrctpqgdwspaaptcevkscdd 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 {\tt fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaklktqtnsdfspgqevfyscepg}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPISQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -rcrrkscrnppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                              64
                                                                                                                                                                                                                                                               repeat; regulator of complement activation;
   /note= "Arg substituted by Lys (SCR-9)"
                                                                         /label= SCR-8
511..543
                                                                                                                                       /label= SCR-1
61..122
                                                        /label= SCR-9
                                                                                                                                                                                    Location/Qualifiers
                                         'note= "TRUNCATED"
                                                                                                                      /label= SCR-2
                                                                       . 543
                                                                                                       .510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19.7%; Score 295.5; DB 13; 26.0%; Pred. No. 4.8e-17; tive 44; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YKCNMG 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig 2 and R11810; 23pp; English
                                   223 YEYSERGDAVCTESG-WRP-LPSCEEKSCDN 251
                                                               229 fvmkgprrvkcqalnkwepelpscsrvcqpppdvlhaertqrdkdnfspgqevfyscepg
                                                                                                                                    169 epsiyctsnddqvgiwsgpapqciipnkctppnvengilvsdnrslfslnevvefrcqpv 228
                                                                                                                                                                                                         113 wdnetpicdripcglppti-tngdfistnre---nfhygsvvtyrcnpgsggrkvfelvg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complement activity regulator protein analogues - useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1992-375009/46.
                                                                                                                                                                         169 DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKEN------
                                                                                                                                                                                                                                               116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-MAY-1991;
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ydlrgaasmrctpqgdwspaaptcevkscdd
                                                                                                                                                                                                                                                                                                                    RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                     cnapewlpfarptnlt----defefpigtylnyecrpgysgrpfsiiclknsvwtgakd- 56
                                                                                                                                                                                                                                                                                                                                                                                       CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                  rcrrkscknppdpvngmvhvikg--iqfgsqikysctkgyrligs-ssatciisgdtvi 112-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hourcade D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                             19.7%; Score 294.5; DB 1 26.3%; Pred. No. 5.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                            45; Mismatches 104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Krych M;
                                                                                                          -----ERFQ--
                                                                                                                                                              1 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13; Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or recombinant
                                                                                                        -YKCNMG
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18;

Search completed: November 21, 2000, 16:43:45 Job time: 284 sec

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000
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 CFAH_HUMAN
CFAH_MOUSE
C4BP_HUMAN
CR1_HUMAN
C4BP_BOVIN
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C4BP_MOUSE
CR2_MOUSE
F13B_HOMAN
CR2_WOUSE
F13B_MOUSE
LEM3_HUMAN
APOH_MOUSE
LEM2_HUMAN
APOH_MOUSE
LEM2_HUMAN
APOH_MOUSE
LEM3_MOUSE
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"Solution structure of the fifth repeat of factor of the complement control protein module.";
Biochemistry 31:3626-3634(1992).
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Barlow P.N., Norman D.G., Steinkasserer A., Horne T.J., Pearce J., Driscoll P.C., Sim B., Campbell I.D.;
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CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION

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een the Swiss Institute of Bioinformatics and the EM
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                                                                                                                   **Pomonstration of an unusual allelic variation of mouse factor H by the complete cDNA sequence of the H.2 allotype.";

J. Immunol. 144:358-362(1990).

-i- FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B)NBB COMPLEX (C5 CONVERTASE) IN THE ALTERNATIVE COMPLEMENT PACHWAY.

-i- POLYMORPHISM: TWO CODOMINANT ALLELES OF FACTOR H ARE PRESENT IN
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                  s SWISS-PROT entry is copyright. It is produced through a collaboratic ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on it
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23-OCT-1986 (Rel. 02, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
Lintin S.J., Lewin A.R., Reid K.B.M.;
"Derivation of the sequence of the signal peptide
"db-binding protein and interspecies cross-hybridi
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                                                                                                                                                             Matsuguchi T., Okamura S., Aso T., Sata T., Niho Y.;
"Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.";
Biochem. Biophys. Res. Commun. 165:138-144(1989).
                                                      SEQUENCE OF 9-81 FROM
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   cross-hybridisation of the C4bp
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CAB51244.1; CAA27839.1;

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TVISUALIZATION OF human C4b-binding protein and its complexes with visualization of human C4b-binding protein and its complexes with vitamin K-dependent protein S and complement protein C4b.";

LPTOC. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).

C -!- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT C4B. IT COMPLETOR THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT CASINAL, WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT COMPLEX CCI. ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN SINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S CONVERTANCE DETO. LINKED COMPONENT.

C -!- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OR A 530 KDA HOWOHEPTAMER OF ALPHA CHAINS OR A 500 KDA COMPLEX OF ALPHA CHAINS OR A 500 KDA CHAINS AND 1 BETA CHAIN. THE CENTRAL BODY OF THE ALPHA CHAINS OR A 500 KDA CHAINS AND 1 BETA CHAIN.
EMBL; M31452; J
EMBL; M62486; J
EMBL; M62475; J
EMBL; M62477; J
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EMBL; M62479; J
EMBL; M62480; J
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"Molecular cloning and characterization of the binding protein, a regulatory protein of the human complement system.";
Biochem. J. 230:133-141(1985).
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TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
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PFAM; PF00084; sushi; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P10998; 1VVC
MIM; 120830; -.
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                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; X02865; CAA26617.1;
A33568; NBHUC4.
                                                                                                                                                                  SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
TSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRP-----YF 327
                                                                                                                                                        TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTF--CIYKRCRHPGE----- 118
                                                                                                                                                                                          100;
                                 L-PSCEEKSCDN-PYIPNGDYS--PLRIK---HRTGDEITYQCRNGFYPAT-RGNTAKC-
                                                                                     KPPPDIRNGRHSGE----ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSP
                                                                                                      LPVTAPENGKIVSSAMEPDREYHFGOAVRFVCNSGYKIEGDEEMHCSDD---
                                                                                                                     --LRNGQVEIKTDLSFGSQIEFSCSEGFFLIGSTTSR-CEVQDRGVGWSHPLPQCEIVKC
                                                                                                                                       FTLTGGNV-----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC
                  SPPACEPNSCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGYKPTTDEPTTVICQ
                                                    PTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVL--RGSSVIHCDADSKWNP
                                                                    PKCVEISCKSPDVINGSPISO-KIIYKENERFQYKCNMGYEYSERGDAV--C-TESGWRP
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29.3%;
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BY SIMILARITY BY SIMILARITY
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Pred. No. 4.6e-20;
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                                                                                                                                                                                                                                     /FTId=VAR_001978.
67E03F2EA85A16DD CRC64;
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X SUSHI (S
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) (GLCNAC. . .).
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BETA CHAIN)
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CR1_HUMAN
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P17927;
01-NOV-1990 (Rel. 1
01-NOV-1990 (Rel. 1
01-NOV-1997 (Rel. 3
EMBL; M11569; A
EMBL; M11618; A
EMBL; M10618; C
EMBL; Y00816; C
EMBL; X05309; C
EMBL; A28507; A.
PIR; A24748; A:
PIR; B24748; B:
PIR; C24748; C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT RECEPTOR TYPE 1 PRECURSOR (C3B/C4B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong W.W., Klickstein L.B., Smith J.A., Weis J.H., Fearon D.T.;
"Identification of a partial cDNA clone for the human receptor for
complement fragments (3b/C4b.";
Proc. Natl. Acad. Sci. U.S.A. 82:7711-7715(1985).

-!- FUNCTION: CR1. PRESENT ON ERYTHROCYTES, LEUKOCYTES, GLOMERULAR
PODOCYTES, AND SPLENIC FOLLICULAR DENDRITIC CELLS, MEDIATES THE
BINDING BY THESE CELLS OF PARTICLES AND IMMUNE COMPLEXES THAT HA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeating domains that are composed of the s characteristics of C3/C4 binding proteins.";
J. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of distinct C3b and C4b recognition sites in the human C3b/C4b receptor (CR1, CD35) by deletion mutagenesis."; J. Exp. Med. 168:1699-1717(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CR1 OR C3BR.
                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klickstein L.B., Wong W.W., Smith J.A., Weis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 503-2039 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human C3b/C4b receptor (CR1). Demonstration of long homologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fearon D.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE;
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                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYST,
MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A
LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A
CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
                                                                                                                                                                                                                                                                                           MISCELLANEOUS: THIS IS THE SEQUENCE OF THE F ALLOTYPE SIMILARITY: CONTAINS 30 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                           SPECIFICITY
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                                                                                                                                                                email to license@isb-sib.ch).
   A28507.
A24748.
B24748.
C24748.
                                                              AAA52297.1; -.; AAA52298.1; -.; AAA52299.1; -.; CAA68755.1; -.; CAA28933.1; -.
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35,
                                                                                                                                                                               license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AND IMMUNE COMPLEXES THAT HAVE
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HSSP; P08603; 1HFI.
MIM; 120620; -.
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SUSHI B1.
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                                   RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG
        -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI
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                                                                    -DEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD-
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BY
                                                                                                                                                Score 350.5;
Pred. No. 2.
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"Bovine C4b binding protein. Molecular cloning of the alpha- and RT "Bovine C4b binding protein S.";

RT formation with protein S.";

RI J. Immunol. 153:4190-4199(1994).

CC C. FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT CC. ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR C4B. CC. (C3BINA), WHICH THEN HYDROLYZES THE CABCEMENT FRAGMENT C4B. IT CC. ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERVASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CC. CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT. CC. SIBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS CC. (BY SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

CC -: SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q28065;
01-NOV-1997
01-NOV-1997
01-NOV-1997
C48-BINDING
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                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                    P10998;
                                                                                                                                                                       PF00084; sushi;
                                                                                                                                                                                                                 Z31693; CAA83498.1;
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                                                                                                                                                       pathway;
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                                                                                                                                                          Plasma;
a; Glycoprotein; Repeat; Sushi; Signal.
BY SIMILARITY.
C4B-BINDING PROTEIN ALPHA CHAIN.
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T 01-NOV-1997 (Rel. 35, Created)

T 01-NOV-1997 (Rel. 35, Last sequence update)

T 01-NOV-1997 (Rel. 36, Last annotation update)

T5-UUL-1998 (Rel. 36, Last annotation update)

T18-RINDING PROTEIN ALPHA CHAIN PRECURSOR.
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                                                                                                                                                                                                                                                                                                                                                 WSDPLPQCIIAKCEPPPTISNGR--HNGGDED-FYTYGSSVTYSCDRDFSMLGKASISCR
                                                                                                                                                                                                                                                                                                                                                                      WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                            KKRCENPGE-----LLNGQVIVKTDYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVV 161
                                                                                                                                                                                                                                                                                                                                                                                                                   KRPCGHPGDTPFGTFTLTGGNV-----FEYGVKAVYTCNEGYQLLGEIN-YRECDTDG--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQ
                                                                                                                                                                                                                                                                               SERGDAV -- C-TESGWR-PLPSCEEKSC-DNPYIPNGDYSPLRIKHRTGDE------
                                                                                                                                                                                                                                                                                                    VENKTIGVWSPSPPSCKKVICVQPVVKDG-----KITSGFGPIYTYQQSIVYACNKGFRL 273
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27.7%;
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INTERCHAIN (WITH BETA CHAIN
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Pred. No. 1.5e-17;
4; Mismatches 142
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BETA CHAIN) (POTENTIAL).
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SEQUENCE FROM N.A. STRAIN-SPRAGUE-DAWLEY; MEDLINE; 97166082.

TISSUE=LIVER; Thern

Α.

Dahlback

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Hillarp A., Wiklund H.,

Rattus norvegicus (Rat). Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;

Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat

Rattus

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J. Immunol. 158:1315-1323(1997)
                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Z50051; CAA90391.1; -. HSSP; P10998; 1VVC.
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        17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               send an email to license@isb-sib.ch).
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SUBJUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAIN SUBJUNIT: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
PPPDLPYALPASEMNQTDFESHTTLRYNCRPGYSRASSSQSLYCKPLGKWQINIA-----
                                                     PPRRNTEILTGSWSDQT-YPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEW---VALNPLR 60
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                                                                                                                          110;
                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                              62266 MW;
                                                                                                                                            16.9%;
27.0%;
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BY
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                                                                                                                                         Score 317; DB 1;
Pred. No. 2.5e-17;
                                                                                                                 Pred. No. 2.566; Mismatches
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SUSHI 2.
SUSHI 3.
SUSHI 4.
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8 X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                              592F0C667ED1E5FF CRC64;
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D (GLCNAC...)
CTCNAC...)
                                                                                                                    128;
                                                                                                                                                                                                                                                                                                                                                                                                                                BETA CHAIN) (POTENTIAL).
BETA CHAIN) (POTENTIAL).
                                                                                                                                                                    Length 558;
                                                                                                              Indels 124;
                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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RESULT 7
C4BP_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                         of the serum complement system.";

Blochemistry 26:4668-4674(1987).

Blochemistry 26:4668-4674(1987).

FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION: OTHER HINDS AS A COFACTOR TO C3B/C4B INACTIVATOR

(C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.

1. SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence u
01-NOV-1997 (Rel. 35, Last annotation
C4B-BINDING PROTEIN PRECURSOR (C4BP).
                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                       EMBL;
                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4BPA OR C4BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kristensen T., Ogata R.T., Chung L.P., Reid K.B.M., "CDNA structure of murine C4b-binding protein, a re-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                   BETA CHAIN OF C4BP.

SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.

SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.

CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-44 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCDYPD-IKHG
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88024997.
                                                                                                    NBMSC4.
                                                                                                                     AAA37312.1; ALT_INIT.
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SIGNAL

Complement pathway; Plasma; Glycoprotein; Repeat;

Sushi;

Signal

PFAM; PF00084; sushi; 6.

MGD; MGI:88229; C4BP.

P10998;

1VVC.

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Best Local S
Matches 94
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CARBOHYD
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REPEAT
                                                                                        CR2_HUMAN STANDARD; PRT; 1033 AA.

P20023;
01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT (EPSTEIN-BARR VIRUS RECEPTOR) (CD21 ANTIGEN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
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                                                      Homo
                                                                        CR2
                                     Eukaryota; Metazoa;
                 Mammalia;
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                                                                        OR C3DR.
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                                                      sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -DDGFWSKEKPKCVEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMGYEYSERGDAVC
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                                                                                                                                                                                                                                                                                                                                     TSTGWI-PAPRCTLKPCDYPDIKHGGLYHE 320
                                                                                                                                                                                                                                                                                                                                                                            QGNGNWSSLPTC-EFDCDLPPAIVNGYYTSMVYSKIT--LVTYECDKG-YRLVGKAIISC
                                                                                                                                                                                                                                                                                                                                                                                                                                                  KTVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVIEC
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                 ; Metazoa; Chordata;
Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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6 X SUSHI (SCR) REPEATS.
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SUSHI 3.
SUSHI 4.
SUSHI 5.
SUSHI 5.
SUSHI 6.
BY SIMILARITY.
BY
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Pred. No. 5.
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                   Catarrhini;
                                     Craniata; Vertebrata; Euteleostomi;
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hes 149;
                   Hominidae;
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 THEFT TETTER AND DESCRIPTION OF THE PROPERTY O
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EMBL; M24010; AAB04638.1; J
EMBL; M24011; AAB04638.1; J
EMBL; M26009; AAB04638.1; J
EMBL; M26010; AAB04638.1; J
EMBL; M26011; AAB04638.1; J
EMBL; M26011; AAB04638.1; J
EMBL; M26013; AAB04638.1; J
EMBL; M26013; AAB04638.1; J
EMBL; M26013; AAB04638.1; J
EMBL; M26014; AAB04638.1; J
EMBL; M26015; AAB04638.1; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Biol. [2]
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Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).

Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).

-I- FUNCTION: RECEPTOR FOR COMPLEMENT C3D AND FOR THE EPST VIRUS ON HUMAN B-CELLS. PARTICIPATES IN B LYMPHOCYTES

-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I- TISSUE SPECIFICITY: MATURE B LYMPHOCYTES AND FOLLICULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Weis J.J., Fearon D.T., Klickstein L.B., Wong W.W., Richards S.A de Bruyn Kops A., Smith J.A., Weis J.H.; "Identification of a partial cDNA clone for the C3d/Epstein-Barr virus receptor of human B lymphocytes: homology with the receptor fragments C3b and C4b of the third and fourth components of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWI
between
                   TRANSMEM
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MEDLINE; 86287311.
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Holers V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 89123277.
                                                                                                                                                                    Receptor;
SIGNAL
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PIR;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE;
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DOMAIN
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                                                                                                                                                                                                                                                                HSSP; P10998
MIM; 120650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European
                                                                                                                                                                                                                           PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE COMPLEMENT ACTIVATION (RCA) FAMILY. SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS. DATABASE: NAME-PROW; NOTE-CD guide CD21 entry; WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD21.HTM"
                                                                                                                                                                                                                                                                                                   A32036;
A24319;
B24319;
C24319;
D24319;
E24319;
F24319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DENDRITIC CELLS OF THE SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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M24008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor.";
ol. Chem. 264:2118-2125(1989).
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M26016; AAB04638.
                                                                                                                                                                                                                                                                                    P10998;
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AAB04638.1;
AAB04638.1;
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AAB04638.
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   SUSHI
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                                                                        CYTOPLASMIC (POTENTIAL)
15 X SUSHI (SCR) REPEAT
                                                                                                                 POTENTIAL
                                                                                                                                   EXTRACELLULAR (POTENTIAL).
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FOLLICULAR THE REGULATORS

EPSTEIN-BARR

ACTIVATION

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511 GTIPWFMEIRLCKEITCPPPPVIYNGAHTGSSLE---DFPYGTTVTYTCNPGPERGVEFS
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                                                                                                      57
                                                                                                                                                               1 EDCNELPPRRNTEILTGSWSDQ----TYPEGTQAIYKCRPGYRSLGNVIMVC-RKGEWVAL 56
                                                                                             NPLRKCQKRPCGHPG----DTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECD 112
                                                                                                                             KEC-QAPP----NILNGQKEDRHMVREDPGTSIKYSCNPGYVLVGEESIQCTSEGVWTP- 461
                               "TDGWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YK 165
                                                                -PVPQCKVAACEATGRQLLTKPQHQFVRPDVN------SSCGEGYKLSGSV-YQECQ 510
                                                                                                                                                                                                                    Similarity
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23.7%;
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N-
                                                                                                                                                                                                    58;
                                                                                                                                                                                                                  Score 307; DB 1
Pred. No. 3e-16;
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SUSHI 11.
SUSHI 11.
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SUSHI 13.
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BY SIMILA
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RESULT 9
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                                                                                                                               molecular linkage to Crry.";

J. Immunol. 143:2058-2067(1989).

-I. FUNCTION: RECEPTOR FOR COMPLEMENT C3D. PARTICI LYMPHOCYTES ACTIVATION.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-I. SIMILARITY: TO HUMAN C3D/EBV RECEPTOR (CD21).

-I. SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CR2_MOUSE P19070;
                                                                                                                                                                                                                                                                                         characterization of the murine homolog (Cr2) to human CR2 and
                                                                                                                                                                                                                                                                                                           Kurtz C.B., Paul M.S., Aegerter M., Weis J.J., Weis J.H.;
"Murine complement receptor gene family. II. Identification and
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 289-1025 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                         Fingeroth J.D., Benedict M.A., Levy D.N., Strominger J.L.; "Identification of murine complement receptor type 2."; proc. Natl. Acad. Sci. U.S.A. 86:242-246(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Molina H., Kinoshita T., Inoue K., Carel J.C., Holers V.M.; "A molecular and immunochemical characterization of mouse CR2. "Evidence for a single gene model of mouse complement receptors 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 343-401 AND 991-1025 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 12-1025 FROM N.A. MEDLINE; 91010789.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
00-FEB-1996 (Rel. 33, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-BALB/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fingeroth J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Comparative structure and evolution of murine CR2. The homolog the human C3d/EBV receptor (CD21).";
J. Immunol. 144:3458-3467(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 90229735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunol. 145:2974-2983(1990)
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EMBL; M81083; AAA374451.1;
EMBL; M35684; AAA37448.1;
EMBL; M61132; AAA63295.1;
EMBL; M35685; AAA37450.1; &
EMBL; M39281; AAA37447.1;
EMBL; M43526; A43526.
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F13B_HUMAN
P05160;
13-AUG-1987
01-AUG-1990
15-JUL-1999
COAGULATION;
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CONFLICT
CONFLICT
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SEQUENCE
                                                                                                                                                                                                                                                                                                                       GLUTAMINE CHAIN).
SEQUENCE OF 2-661 FROM N.A.

SEQUENCE OF 2-661 FROM N.A.

MEDLINE; 87026535.

TChinose A., McMullen B.A., Fujikawa K
"Amino acid sequence of the b subunit composed of ten repetitive segments.";

Biochemistry 25:4633-4638(1986).
                                                                                                                                                                                              SEQUENCE;
                                                                                                                                                                                                                                                  Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                          Biochemistry
                                                                                                                                                             "Nucleotide sequence
                                                                                                                                                                                 Bottenus
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96; Conser
                                                                                                                                                                              FROM N.A.
91105054.
R.E., Ich
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90 (Rel. 15, Last sequence update)
99 (Rel. 3B, Last annotation update)
99 (Rel. 3B, Last annotation (EC
ON FACTOR XIII B CHAIN PRECURSOR (EC
GAMMA-GLUTAMYLTRANSFERASE B CHAIN)
                                                                                                                                                                                                                                                    Eutheria;
                                                                                                                                                                                                                                                                     Metazoa;
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equence of
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YGS -> EFR (IN REF. 2)
YGS -> A (IN REF. 2)
P -> A (IN REF. 2)
P -> A (IN REF. 2)
MISSING (IN REF. 2)
MISSING (IN REF. 4)
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7; Mismatches
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                                        Ø
                                        protein
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MIM; 134580;
                                                                                                                                                                                                                                                                                                      EMBL; M64554; AAA51821.1; ALT_SEQ.

EMBL; M14057; AAA88042.1; -.

EMBL; X51823; CAA36123.1; -.

PIR; A23830; A23830.

PIR; A36397; A36397.

PIR; A36397; A36397.

PIR; S09980; S09980.
                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                 REPEAT
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                                                                                                                                                                                                                                                             Transferase;
                                                                                                                                                                                                                                                                    PFAM; PF00084;
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- IFUNCTION: THE B CHAIN OF FACTOR XIII IS NO
BUT IS THOUGHT TO STABILIZE THE A SUBUNITS
OF TRANSGLUTAMINASE FORMATION BY THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Grundmann U., Nerlich C., Rein T., Zettlmeissl G.; "Complete cDNA sequence encoding the B subunit of human Nucleic Acids Res. 18:2817-2817(1990).
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REVISIONS.
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                                                                                                                                                                                                                                                                               NTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS. DISEASE: A DEFICIENCY IN FA13 CAN RESULT IN A LIFELONG TENDENCY, DEFECTIVE WOUND HEALING, AND HABITUAL ABORTIC SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                    .; Disease
                                                                                                                                                                                                                                                                                               P08603; 1HFI.
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netic defects in a patient with complete
for coagulation factor XIII.";
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  Plasma; Blood
                                                                                                                                                                                                                                                                    sushi;
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 N.A.
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                                                                                                                                                                                                                        (SCR)
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VCP_VACCV STANDARD; PRT; 263 AA. P10998; 01-JUL-1989 (Rel. 11, Created) 01-JUL-1989 (Rel. 11, Last sequence update) 15-JUL-1998 (Rel. 36, Last annotation update) COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY
                                                  MREDLINE; 89073756.

Kotwal G.J., Moss B.;

Nanalysis of a large cluster of nonessential vaccinia virus terminal transposition mutant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID DISULFID
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Kotwal G.J.,
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SITE
                            Virology 167:524-537(1988)
                                                                                                                                                                                                     STRAIN-WR;
                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               "Vaccinia virus encodes a secreto to complement control proteins."; Nature 335:176-178(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-WR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Orthopoxvirus.
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C -> F (IN F13B DEFICIENCY).
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57A2FB46560857F2 CRC64;
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3.7e-16,
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Vaccinia virus complement-control protein prevents antibody-dependent complement-enhanced neutralization and contributes to virulence.";
                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE BY NMR OF 146-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paoletti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Barlow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wiles A.P., Shaw G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Goebel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                      PFAM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [saacs S.N.,
                                                                                                                                                                                                                                                                                                                                                    PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
INTERPRO; IPR000436; -
PFAM; PF00084; sushi; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NMR studies of a viral protein that mimics the regulators of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF CONACTIVATION. BINDS C3B AND C4B.
SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS COMPLEMENT ACTIVATION (RCA).
SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JLEMENT ACTIVATION.";
JLEMENT ACTIVATION.";
MOI. Biol. 272:253-265(1997).
FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY
FUNCTION: STRUES TO PROTECT AND ALTERNATIVE PATHWAYS OF COMPLEMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete DNA sequence of vaccinia logy 179:247-266(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                 A31005; WMVZSP.
1VVC; 03-DEC-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.J., Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.J., Johnson G.P.,
                                                                                                                                                                                                                                                                                                                               Repeat;
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                                                                                                                                                                                                                                                                                                                                 Sushi;
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                                                                                                                                                                                                                                                                                                                                 3D-structure
      WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perkus M.E.,
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                     4 X SUSI
SUSHI 1
SUSHI 2
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SUSHI 4
BY SIMII
                                                                                                                                                                                                                                                                   COMPLEMENT CONTROL PROTEIN. 4 X SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89:628-632(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                В.
                     Y SIMILARITY.
      E4322CC9A6EF8997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perczel A.,
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E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Winslow J.P.,
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Query Match

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q07968;
01-FEB-1995
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
COAGULATION FACTOR XIII B CHAIN PRECURSOR (EC 2.3.2.13) (PROTEIN-GLUTAMINE GAMMA-GLUTAMYLTRANSFERASE B CHAIN) (TRANSGLUTAMINASE B
                                                                                                                Sushi.
SIGNAL
                     REPEAT
REPEAT
                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and assignment of the gene to chromosome relationship to complement factor H."; Genomics 15:535-542(1993).
                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The second of the s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nonaka M., Matsuda Y., Shiroishi T., Natsuume-Sakai S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-B10.D2/OSN;
MEDLINE; 93224141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F13B_MOUSE
                                                                    DOMAIN
                                                                                                                                                         Transferase;
                                                                                                                                                                                                                                MGD; MGI:88379; F13B.
                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                              PIR; A46013; A46013.
                                                                                                                                                                                                                                                                                                       EMBL; D10071; BAA00963.1;
                                                                                                                                                                                                                                                                                                                                                                                               modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Molecular cloning of the b subunit of mouse
                                                                                                                                                                                                          INTERPRO; IPRO00436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: THE B CHAIN OF FACTOR XIII IS NOT CATALYTICALLY BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND REGULATE THE OF TRANSGLUTAMINASE FORMATION BY THROMBIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS. TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISNGR--HNGYED--FYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-DPPTCQIVKCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---WTNDIPICEVVKCLPVTA 133
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                                                                                                                                                                                       PF00084;
                                                                                                                                                                                                                                                         P10998; 1VVC
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Eutheria;
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etazoa; Chordata;
theria; Rodentia;
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                                                                                                                                                                             . sushi; 8
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                                                                                                                                                                 Blood
                                                                                                                                                              coagulation;
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9; Mismatches 106;
COAGULATION FACTOR XIII B
10 X SUSHI (SCR) REPEATS.
SUSHI 1.
SUSHI 1.
SUSHI 2.
SUSHI 3.
                                                                                                                  BY SIMILARITY
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Moriwaki K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 668
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thi; Muridae; Murinae; Mus
                                                                                                                                                                 Repeat; Glycoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                     There are no rest
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            coagulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   evolutionary
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                                                                                                                                                                                                                                                                                                                                                                                                                                             restrictions
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                                                            LEM3. HUMAN STANDARD; FRI, CEM3. HUMAN STANDARD, FRI, CEM3. 
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                                                                                                                                                                                                                                                                                                                                                                          KGSETSRCEQGAWSSPPVC-LEPCTI-DVDH 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTITCNRGRWTLPPECVENIENCKPPPDIANGVVVDGLLASYTTGSSVEYRC-NEYYLL 431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WINDIPICE--VVKCLPVTAPENGKIVSSAMEP-DREYHFGQAVRFVCNSGYKIEGDEEM 172
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Pred. No. 1.8e-15;
               Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 668;
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                PTO715 allele carriers in patients with myocardial infarction.",

Hum. Mol. Genet. 7:1277-1284(1998).

-i. FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT BINDS

TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE

INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH

LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.

-i. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

-i. TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS

AND WEIBEL-PALADE BODIES OF ENDOTHELIAL CELLS. UPON CELL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
[5]
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Bajorath J., Stenkamp R., Aruffo A.;
"Knowledge-based model building of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of GMP-140, a granule membrane protein of platelets and endothelium: sequence similarity to proteins involved in cell adhesion and inflammation."; Cell 56:1033-1044(1989).
                                                                                                                                EMBL;
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J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fujimoto T., Stroud E., Whatley R.E., Prescott S.M., Muszbek L., Laposata M., McEver R.P.;
"P-selectin is acylated with palmitic acid and stearic acid at cysteine 766 through a thioester linkage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ruidavets J.B., Arveiler D., Luc G., Cambien F.; "The P-selectin gene is highly polymorphic: reduced frequency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Herrmann S.M., Ricard S., Nicaud V., Mallet C., Evans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VARIANTS ASN-331; ASP-603; VAL-640 AND PRO-756, MEDLINE; 98334547.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochemistry 35:13733-13744(1996).
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MEDLINE; 93266599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure and function of the epidermal growth factor domain of P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
[1]
                                                                                                                                                                                                                                                                                                                                  SIMILARITY: TO OTHER SELECTINS/LECAMS
SIMILARITY: CONTAINS 1 C-TYPE LECTIN I
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN
SIMILARITY: CONTAINS 9 SUSHI (SCR) REI
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                                                                                                                                                                                                                                                                                                                     DATABASE: NAME=PROW;
                                                                                                                                                                                                                                                                                                    DATABASE: NAME-PROW; NOTE-CD guide CD62P entry; WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD62P.HTM".
                                                                                                                                                                                                                                                                                                                                                                                                               ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
M60234;
M60217;
M602218;
M602223;
M60223;
M60224;
M60224;
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                                              AAA35910.
AAA35910.
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1 EGF-LIKE DOMAIN.
9 SUSHI (SCR) REPEATS.
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PROSITE; PS001865 EGF_1; 1.

PROSITE; PS011865 EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS0041; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; ECCell adhesion; Transmembrane; Lipoprotein; ECCell adhesion; Signal; Sushi; Repeat; Lipoprotein;
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A30359; A
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1KJD; 03-APR-96
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IPR000561; -.
IPR001304; -.
IPR002396; -.
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C-TYPE LECTIN (SHORT FO
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Best Local :
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LIPID
                                                                                                                                                                            Genomics [2]
                                                                                                                                                                                                                                                                                                                                                                                                            APOH_MOUSE STANDARD; PRT; 345 AA. (201339; Q01339; Q1-APR-1993 (Rel. 25, Created) Q1-APR-1993 (Rel. 25, Last sequence update) Q1-OCT-2000 (Rel. 40, Last annotation update) BETA-Z-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (BETA(2)GPI) (ACTIVATED PROTEIN C-BINDING PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARIANT
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Biochem.
[3]
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                                    "Characterization, expression and evolution glycoprotein I (apolipoprotein H).";
                                                                         STRAIN-CBAJ; TISSUE-LIVER;
STRAIN-CBAJ; TISSUE-LIVER;
MEDLINE; 94/24/2017.
Sellar G.C., Steel D.M., Zafiropoulos
Whitehead A.S.;
                                                                                                                                                                                                                 Nonaka M., Matsuda
"Molecular cloning
gene to chromosome
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                                                                                                                                                                                                                                                                                               SEQUENCE
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musculus (Mouse).
musculus (Mouse).
rwota; Metazoa; Chordata;
rworia; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {\tt GSSCKFECQPGYRVRGLDMLRCIDSGHWSA--PLPTCEAISC-EPLESPVHGSMDCSPSL}
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                  Biophys.
                                                                                                                                                                                             13:1082-1087(1992).
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29.6%;
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N-LINKED
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Pred. No. 9.
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/FTId-YAR_004195.
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                                                                                                                                                                                                                                                                                                                                    Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FBC407BA2579F6EB CRC64;
                      200:1521-1528(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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2-glycoprotein
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(GLCNAC.)
(GLCNAC.)
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                                                                                                  Α.,
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thi; Muridae;
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.6e-15;
                                                                                                Seery L.T.,
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Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Structure of the human beta-2-glycoprotein I gene.";
Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: BINDS TO VARIOUS KINDS OF NEGATIVELY CHARGED SUBSTANCES
SUCH AS HEPARIN, PHOSPHOLIPIDS, AND DEXTRAN SULFATE. MAY PREVENT
ACTIVATION OF THE INTRINSIC BLOOD COAGULATION CASCADE BY BINDING
TO PHOSPHOLIPIDS ON THE SURFACE OF DAMAGED CELLS.
                                   154
                                                                140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
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STRAIN=BALB/C; TISSUE=LIVER;
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                                                                                                                                                                                                                   Local Similarity
NG---SPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRPLPSCEEKSCDNPYI
                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collab ween the Swiss Institute of Bioinformatics and the EMBI outst European Bioinformatics Institute. There are no restrictions by non-profit institutions as long as its content is in ified and this statement is not removed. Usage by and for comparing the statement is not removed.
                             KDYRPSAGNNSLYQDTVVFKCLPHFAMIGNDTVMCTEQGNWTR-LPECLEVKCPFPPRPE
                                                      VSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK-SPDVI 198
                                                                                  TS---FEYPKNISFACNPGFFLNG-TSSSKCTEEGKWSPDIPACARITCPPPPPVPKFALL
                                                                                                           TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVKCLPVTAPENGKI 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                          SYDPGEQIVYSCKPGYVSRGGMRRFTCPLTGMW-PINTLR-CVPRVCPFAGILENGIVRY
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S70439;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR000436;
                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                        38619
                                                                                                                                                                                                14.9%; Score 279.5; DB 1
27.7%; Pred. No. 1.1e-14;
tive 44; Mismatches 132
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OF COLONA

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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
G -> R (IN REF. 2).
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SUSHI 2.
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                     Graves B.J., Crowther R.L., Chandran C., Rumberger J.M., Li S., Huang K.-S., Presky D.H., Familletti P.C., Wolitzky B.A., Burns D.K.; "Insight into E-selectin/ligand interaction from the crystal structure and mutagenesis of the lec/EGF domains."; nature 367:532-538(1994).
                  Nature
VARIANT ARG-149.
                                                                                                MEDLINE; 94150646
                                                                                                                                                                                                                                                                                                                                                       Collins T., Williams A., Johnston G.I., Kim Gimbrone M.A. Jr., Bevilacqua M.P.; "Structure and chromosomal location of the leukocyte_adhesion_molecule_1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P16581; P16111;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 15, Last sequence update)
15-JUL-1990 (Rel. 38, Last annotation update)
15-JUL-1999 (Rel. 38, Last annotation update)
5-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1)
(ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM-
                                                                                                                                                                                                                                                                 Phillips M.L., Nudelman E., Gaeta F.C., Perez M., Singhal A.K., Hakomori S., Paulson J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bevilacqua M.P., Stengelin S., Gimbrone M.A. Jr., Seed B.; "Endothelial leukocyte adhesion molecule 1: an inducible receptor neutrophils related to complement regulatory proteins and lectins. Science 243:1160-1165(1989).
                                                                                                                                                                       Mills A.;
                                                                                                                                                                                       MEDLINE; 93202275
                                                                                                                                                                                                                              Science
                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE;
                                                                                                                                                      "Modelling the carbohydrate recognition domain of human
                                                                                                                                                                                                  3D-STRUCTURE MODELING
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                                                                                                                                                                                                                                                          "ELAM-1 mediates cell adhesion by
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                                                                                                            -RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF
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C., Osborn L.,
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Tizard R., Goelz S., McCarthy
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Carthy K., Ho
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PFAM; PF00008; EGF; 1.

PFAM; PF000089; lectin_c; 1.

PFAM; PF00084; sushi; 6.

PRINTS; PR00343; SELECTIN.

PROSITE; PS00022; EGF_1; 1.

PROSITE; PS01186; EGF_2; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; 1.

PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

Cell adhesion; Transmembrane; Glycoprotein; EG
Selectin; Signal; Sushi; Repeat; Polymorphism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE; 95179107.
Wenzel K., Felix S., Kleber F.X., Brachold R., Menke T., Schulte K.L., Glaser C., Rohde K., Baumann G., Speer A.; "E-selectin polymorphism and atherosclerosis: an associat Hum. Mol. Genet. 3:1935-1937(1994).
                                                                                                                                                                                                                                                                                                         PDB; 1ESL; 31
PDB; 1KJA; 03
MIM; 131210;
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INTERPRO; IPRO02396;
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S.Q., Usher D., Virgil D., Zhang L.Q., Yochim S.E., Gupta F.
Polymorphism detects the mutation of serine-128 to arg
serine-128 to arg
holder serine-128 to arg
holder of coronary artery disease.";
Biomed. Sci. 6:18-21(1999).

FUNCTION: EXPRESSED ON CYTOKINE INDUCED ENDOTHELIAL CELLS
MEDIATES THEIR BINDING TO LEUKOCYTES. THE LIGAND RECOGNIZE
ELAM-1 IS SIALYL-LEWIS X (ALPHA(1->3)FUCOSYLATED DERIVATIV
POLYLACTOSAMINE THAT ARE FOUND AT THE NONREDUCING TERMINI
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SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
DATABASE: NAME-PROW; NOTE-CD guide CD62E entry;
WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD62E.HTM"
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SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.

POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH POLYMORPHISM: A POLYMORPHISM IN POSITION 149 IS ASSOCIATED WITH HIGHER RISK OF CORONARY ARTERY DISEASE (CAD). A SIGNIFICANTLY HIGHER MUTATION FREQUENCY (ARG-149) IS OBSERVED IN PATIENTS WITH ANGIOGRAPHICALLY PROVEN SEVERE ATHEROSCLEROSIS COMPARED WITH AN UNSELECTED POLYMING (SER-149).
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, M61893; AAA52375.1;
, M61895; AAA52375.1;
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A35046; A35046.
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C-TYPE LECTIN (SHORT FORM)
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                             WIPAPRCTLKPCDYP
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	80	7	6	5	4	ω	N	1	Result
323	328	328	333.5	335	337.5	339	342.5	348	349.5	350.5	350.5	350.5	351	353	377	486	903	1876	Score
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11	12	12	6	12	Ģ	δ	6	σ	12	4	4	4	6	11	6	13	6	4	BB
Q63612	040912	P88903	Q28770	Q9YTQ8	Q22328	Q28797	Q29531	Q29530	Q9WRU2	Q16744	Q16745	Q9UQV2	Q29528	Q99254	Q28769	Q91275	Q28085	Q14570	Ħ
Q63612 rattus norv		P88903 kaposi's sa	Q28770 papio hamad	Q9ytq8 ateline her	Q22328 caenorhabdi	Q28797 pan troglod		Q29530 pan troglod	Q9wru2 macaca mula	Q16744 homo sapien	Q16745 homo sapien	Q9uqv2 homo sapien	Q29528 papio hamad	Q99254 mus musculu	Q28769 papio hamad	Q91275 paralabrax	Q28085 bos taurus	Q14570 homo sapien	Description

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308.5 308.5 308.5 302.5 302.5 302.5 292.9 298.3 299.8 288.3 298.3 297.2 272.7 272.7 572.7	323 317 310
16.3 16.3 16.1 16.1 15.0 15.0 15.0 15.0 15.0 16.1 11.0 15.0 10.0 11.0 11.0 11.0 11.0 11	17.2 16.9 16.5
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013866 035520 061405 0404735 014069 008569 008569 004839 0048545 014612 060736 089859 07073 09703 095508 916976 916976 91611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611 091611	Q63135 Q61407 P87616
Q13866 homo sapien Q1386 homo sapien Q136775 mus musculu Q61405 mus musculu Q14006 homo sapien Q08569 cavia porce Q9vyr4 drosophila Q9viu9 drosophila Q9viu9 drosophila Q02839 sus scrofa Q46545 ovis aries Q14212 homo sapien Q60736 mus musculu Q89859 variola vir Q907033 variola vir Q907033 variola vir Q91568 drosophila Q89061 variola vir Q9u611 drosophila Q15429 homo sapien Q15427 macaca fasc Q19127 macaca mula p79138 cercopithec	

ALIGNMENTS

FF	DR	DR	DR	DR	DR	DR	DR	RI.	RA	RP	R	RL	R.P.	RP	RN	RL	RΤ	RT	RA	RX	RP	Z	RL	RT	RA	RX	RΡ	RN	გ	8	SO	GN	DΕ	DΤ	D.J.	DΤ	AC	ID	014570	RESULT	
SIGNAL 1 18 POTENTIAL.	PFAM; PF00084; sushi; 7.	00436; -	P10998;	Z29665;	U56979; AAB01987.	M12383; AAA52013	k07523; CAA30403.1;		z O.;	SEQUENCE OF 1-9 FROM N.A.			, Willia	SEQUENCE OF 1-19 FROM N.A.	_	3407-3411(1986).	glycoprotein I, and the Ba f	of human complement protein H: homology with	Kristensen T., Wetsel R.A., Tack B.F.;	86169701.	SEQUENCE OF 226-449 FROM N.A.		•	mplete amino acid sequence of huma	ч		SEQUENCE FROM N.A.	[1]	Primates;	m	Homo sapiens (Human).		FACTOR H PRECURSOR.	(TrEMBLrel. 13, Last annotation	(TrEMBLrel. 01,	\vdash	Q14570; P78435;	Q14570 PRELIMINARY; PRT; 449 AA.	70	LT 1	

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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                    INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 11.
                                                                                                                                                                                                                                                                 Soames C.J., Day A.J., Sim R.B.;
"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
EMBL; X98697; CAA67257.1; -.
HSSP; P1099B; IVVC.
                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Bos taurus (Bovine).

Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q28085;
                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                        TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                  136
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                                                                                                                                    Local Similarity
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 NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                          GTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPE 135
                              NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP 195
                                                         GSPHLAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCTLKPCDYPDIKHGGLYHENMRRPYFPV 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                    96202005.
                                                                                                                                                                                            669
669 AA;
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449 i
                                                                                                                      Conservative
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75683 MW;
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51033 MW;
                                                                                                                                  48.1%; Score 903; DB 6; 60.9%; Pred. No. 3.8e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .0%; Score 1876; DB 4; .0%; Pred. No. 6.8e-161;
                                                                                                                   33; Mismatches
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                                                                                                                                                                                           D0D9DB30EE747AC2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2AAD47F155343E3 CRC64;
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                                                                                                                                              Length 669,
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Q91275;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 13, Last annotation update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT REGULATORY PLASMA PROTEIN.
COMPLEMENT REGULATORY PLASMA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L21703; AAA92556.1; HSSP; P08603; 1HFH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTY ....;
neblifer).";
netochem. J. 301:391-397(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE; 94318039.

Dahmen A., Kaidoh T., Zipfel P.F., Gigli I.;

"Cloning and characterization of a cDNA representing a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Paralabrax nebulifer (barred sand bass).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
Percomorpha; Perciformes; Percoidei; Serranidae; Paralabrax.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement-regulatory plasma protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO;
 397
                                310 PDIKHG-----GLYHENMRRPY 326
                                                              338 RPEHVDSWDVRSWERYTLDDNTRYWCKRG-YKRTGGVTWATCGRNGWMPNPLCEVKTCSK 396
                                                                                                                                        278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 DVINGSPISQKIIYKENERPQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP
                                                                                                                                                                                                                                                                                                                                                                             81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :SSUE=LIVER;
ENIQDAVIVGTDKQIYNLNQKAIY 420
                                                                                                                                  GTRYEPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRCSNR
                                                                                                                                                                                                                                                                                                                                                             TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                           DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                    GNVPGAIREYKENDVLHYECDRAFKHIDR-PSTCIKQGIKAEWSPTPLCESIKCRLTIMD
                                                                                                                                                                                                                                      GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG----WRPLPSCEEKSC-----
                                                                                                                                                                                                                                                                                                         SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                         AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQCPLIHVDNNVQVI 162
                                                                                                                                                                                                                                                                                                                                                                                                           EASYPGGRQVRVGCNVGYS--GFFKLVCVEGKWETRG--AKCQPRSCGHPGDAQFADFHL 102
                                                                                                -PLRI-----KHRTGDEITYQCRNGFYPATRGNT-AKCTSTGWIPAPRCTLKPCDY 309
                                                                                                                                                                      ------DNPYIP-----
                                                                                                                                                                                                                                                                       GG----PEEATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114;
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29.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 486; DB 13; Length 1053; Pred. No. 2.1e-35;
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                                                                                                                                                                                                                                                                                                                     망
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                      099254;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAY-2000 (TrEMBLrel. 13,
COMPLEMENT RECEPTOR TYPE 2 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Birmingham D.J., Logar C.M., Shen X.P., Chen W
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ
EMBL; L77977; AAA99004.1; -
HSSP; P08603; 1HFT.
INTERPRO; IPR000436; -
PPAM; PF00084; sushi; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-NAY-2000 (TrEMBLrel. 13, Last annotation
COMPLEMENT RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                          CR2.
Mus musculus (Mouse).
Mus musculus (Mouse).
Chordata;
                                                                                                                                                                                            Q99254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. TISSUE-BONE MARROW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papio hamadryas (Hamadryas baboon)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q28769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q28769
MEDLINE; 90229754.
Kurtz C.B., O'Toole
                           STRAIN-BALB/C
                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      103
                                                                                                                                                                                                                                                                                                                     274
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                                                                                                                                                                                                                                                                                                                     GFVMKGPRHVQCQALNKWEPELPSCSRVCQPPPEILHGEHTPSHQDFSPGQEVFYSCEPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CN---ELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                            GEPSIYCTSKDDQVGIWSGPAPQCIIPNKCMPPNVENGVLVSVNRSLFSLNEVVEFRCQP
                                                                                                                                                                                                                                                                                                                                                                                                                                 WDNETPICETIPCGLPPTI-ANGDFISTS----REYFPYGSVVTYRCNLGSGRKKLFELV
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSG-----YKIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNAPEQLPFARPTNLTDAS----EFPVGTYLKYECLPGYHGKPFSIICLKNSVWTSAKD-
                                                                                                                                                                                                                                                                                          FYPATRGNTAKCTSTG-WIP-APRCTLKPCD--YPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                     GYEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNG
                                                                                                                                                                                                                                                                                                                                                                                             GDEEMHCS--DD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -KCTRKSCRNPKDPVNGMVHVI--KDIQFGSQINYSCNKGYRLIGS-SSATCIISGNTVI 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107;
                                                                                                                                                                                                                                                                -YDLRGAASLHCTPQGDWNPEAPICTVKSCDDFLGQLPHG-----
                                                                   Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    522 AA;
                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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 E
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                                                                   Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.1%;
 Christensen
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                                                                                                                       (CR2) (FRAGMENT).
                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 377; DB 6; Pred. No. 5.8e-26;
                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    312FCBE03ADF19DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence update)
S.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                   Murinae; Mus
                                                                                                                                                                                                                                                              RVLFPL 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           167
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                                                                                                                                                                                                                                                                                                                             B
 Query Match
Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cofactor protein."
J. Exp. Med. 181:1
EMBL; U17128; AAA7
EMBL; U17124; AAA7
EMBL; U17124; AAA7
EMBL; U17125; AAA7
EMBL; U17125; AAA7
EMBL; U17126; AAA7
EMBL; U17127; AAA7
EMBL; U17127; AAA7
EMBL; W17127; AAA7
EMBL; W17127; AAA7
EMBL; W17127; AAA7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE; 9
Kim Y.U.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1."; J. Immunol. 144:3581-3591(1990).
                                                                                                     COMPLEMENT RECEPTOR CR1.
                                                                                                                               Q29528 PRELIMINARY; PRT; 1911 AA. Q29528; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of both human decay-accelerating factor and membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
SEQUENCE FROM N.A. Clemenza L., Subra
                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Holers V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:88489; Cr2.
                                           Cercopithecinae;
                                                                                    Papio hamadryas (Hamadryas baboon).
                                                                                                                                                                                                                                                                     328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SNGDFYSSSRD---SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDGWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDOT-YPEGTOAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCOKRPCGHPGDTPFGTF 78
                                                                                                                                                                                                                                                                    VPTCEVKSCDAIPNHLLHGRVF
                                                                                                                                                                                                                                                                                                                           \verb|LPTCFMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNT|\\
                                                                                                                                                                                                                                                                                                                                                        LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG-WI-P
                                                                                                                                                                                                                                                                                                                                                                                      PQCIPRVKCPMPEIENGLVESGFKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPP
                                                                                                                                                                                                                                                                                                                                                                                                                 PKCV-EISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWR-P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCSDD-----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HINTG--IEFGSTITYSCNQGYRLIGD-SSATCIVSDNTVMWDNDMPLCESIPCESPPAI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDKSEFAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    679 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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 Subramanian
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                                            Papio
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                                                                                                                   1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    74916 MW;
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 B.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
                                                                                                                                                                                                                                                                     349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 353; DB 11;
Pred. No. 1.1e-23;
                                                          Catarrhini;
                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52FC00FDCED20CDC CRC64;
 Nickells
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 M. W.
                                                          Cercopithecidae
   Hourcade
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seya
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Г.м.,
                                                                                                                                                                                                                                                                                                                                                                                         268
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RESULT
Q9UQV2
   ACC DATE ACC
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Best Local
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HUMAN CRI MRNA FOR C3B/C4B RECEPTOR SECRETED FORM PRECURSOR (FRAGMENT).
                                                         NON_TER
                                                                                                                                                                                                                                                          "Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1.", Exp. Med. 168:1255-1270(1988).

EMBL; X14362; CAA32541.1;
   SEQUENCE
                                  CHAIN
                                                                                                                        Signal
                                                                                                                                                  PFAM; PF00084; sushi; PROSITE; PS00133; CAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE; 89010527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UQV2
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PFAM; PF00084; Sushi; 29.

PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_4.

RON_TER 1911 1911
                                                                                                                                                                                                              INTERPRO; IPR000436; -. INTERPRO; IPR000834; -.
                                                                                                                                                                                                                                                                                                                                                                                                                         Hourcade D., Miesner D.R., Atkinson J.P., Holers V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkinson J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                184 KPKCVEIS-CKSPDVINGSPI-SQKIIYKENERFQYKCNMGYEYSERGDAVC-TESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 SDQTYPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-APRCTLKPCD--YPDIKHG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLPHCSRVCOPPPEILHGEHTPSHQDKFSPGQEVFYSCEPG-YDLRGAASLHCTPQGDWS 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -LPSCEEKSCDNPYIPNGDYSPL-RIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG-WI 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPRCISTNKCTAPEVKNGIRVPGNRSFFSLNEIVRFRCQPGFVMVGSHTVQCQTNNRWGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISNGDFYSNNR----TSFHSGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGAWSSP 1468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCS--DD--GFWSKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVHINTDT-QFGSTVNYSCNEGFRLIGSPS-TTCLVSGNNVTWDKEAPICEIISCKPPPT 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NDFEFPVGTSLNYECHPGY--FGRMFSISCLENLVWSSVED--NCRRKSCGTPPE-PFNG 1353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93;
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   559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1911 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                         <u>^</u>
                                                                                                                                              CARBOXYPEPT_ZN_2; UNKNOWN_1.
   61424 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           210173 MW; 535A4DD0EAFA521D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.7%;
29.0%;
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; Pred. No. 6.1e-23;
57; Mismatches 135;
                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
DBFFE965CA179D75 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 AA.
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RESULT
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Q16745;
Q1-NOY-1996 (TrEMBLrel. 01, Created)
01-NOY-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                     EMBL;
                                                                                           EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
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                                         EMBL;
                                                                             EMBL;
                                                                                                                                                                                                                                   EMBL; L17418; AAB60694.1;
EMBL; L17390; AAB60694.1;
EMBL; L17391; AAB60694.1;
                                                                                                                                                                                                                                                                        Vik D.P., Wong W.W.;
Submitted (JUN-1993)
                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 18.7%;
Local Similarity 29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVMKGPRRVKCQALNKWEPELPSC-SRVCQPP--PDVLHAERTQRDKDNFSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEEMHC -- SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100;
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             AAB60694
AAB60694
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AAB60694
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
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JOINED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 350.5; DB 4;
Pred. No. 1.5e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
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RESULT
Q16744
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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HSSP; P086
INTERPRO;
INTERPRO;
                              SEQUENCE FROM N.A.
MEDLINE; 94065175.
Vik D.P., Wong W.W.;
"Structure of the gene for the F allele of and sequence of the coding region unique to J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
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EMBL;
EMBL;
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01-NOV-1996 (TremBLrel.
01-MAY-2000 (TremBLrel.
COMPLEMENT RECEPTOR 1.
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SEQUENCE FROM N.A. Vik D.P., Wong W.W.;
                                                                                                                                                                                      Q16744
                                                                                                     Mammalia;
                                                                                                                Eukaryota;
                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                             Q16744;
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RPRO; IPR000834; -.
RPRO; IPR001424; -.
RPRO; IPR001424; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CNE----LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
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                                                                                                                                                                                                                                                                                FVMKGPRRVKCQALNKWEPELPSC-SRVCQPP-
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L17411;
L17412;
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PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PS00133; CARBOXYPEPT_ZN_2; UNKNO
                                                                                                     Eutheria;
                                                                                                               Metazoa;
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Primates;
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29.3%;
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Last sequence update)
Last annotation update)
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Pred.
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                                                                                                     Hominidae;
                                         complement receptor type o the S allele.";
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                                                                                                               Euteleostomi;
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EMB
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Best Local Sin
Matches 100;
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EMBL; L17418; AAB60695.1
EMBL; L17390; AAB60695.1
EMBL; L17391; AAB60695.1
EMBL; L17392; AAB60695.1
EMBL; L17393; AAB60695.1
EMBL; L17393; AAB60695.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
EMBL;
EMBL;
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INTERPRO;
                        223
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CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
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L17406;
L17407;
L17408;
L17409;
L17410;
L174112;
L174112;
L17413;
L17414;
L17414;
L17414;
L17414;
L17414;
L17414;
L17414;
L17414;
L17414;
                                                              EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPG
                                                                                    DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                                                          WTNDIPICEVVKC-LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEG
                                                                                                                                                                                                                                  -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI
                                                                                                                                                                                                                                                                                                                       CNAPEWLPFARPTNLT----DEFEFPIGTYLNYECRPGYSGRPFSIICLKNSVWTGAKD-
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P08603;
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L17401;
L17402;
L17403;
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L17395;
L17396;
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17399;
                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; IPRO00436; -.; IPRO00834; -.; IPRO01424; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               00084; sushi; 37.
ps00087; sop_cu_zn_1; unknown_1
ps00133; CARBOXYPEPT_ZN_2; UNKNO
2489 AA; 272846 MW; CEE11B5
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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AAB60695.1
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AAB60695.1;
AAB60695.1;
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AAB60695.
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AAB60695.
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JO
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                                                                                                                                                                                                                                                                                                                                                                                                           55;
                                                                                                                                                                                                                                                                                                                                                                                                     Score 350.5; I
Pred. No. 9.3e
55; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _ZN_2; UNKNOWN_3.
W; CEE11B53F2B4FAF6
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                    GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                     2489;
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RESULT
Q29530
ID Q2
AC Q2
DT 01
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Q9WRU2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
         Q29530;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation updat
                                                                           Q29530
 COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF083501; AAD21332.1; -. INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2000 (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity to Kaposi's sarcoma-associated herpesvirus/human
herpesvirus 8.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Macaca mulatta rhadinovirus 17577.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENT BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9WRU2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searles R.P., Bergquam E.P., Axthelm M.K., Wong S.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9WRU2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence and genomic analysis of a Rhesus macaque rhadinovirus with
                                                                                                                                                          371
                                                                                                                                                                                       298
                                                                                                                                                                                                                                                                                 251
                                                                                                                                                                                                                                                                                                                                           191
                                                                                                                                                                                                                                                                                                                                                                                                        136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMV--CRKGEWVALNP
                                                                                                                                                                                                                                                                            LTCTNTTWVPPLPKCVLVTNNPSTPMPETPMPETPTPDYQKINLSTAKTATTPNAFVTTV 310
                                                                                                                                                        TAPNAKCHRKKCPTPQELLNGEY 393
                                                                                                                                                                                     PAP--RCTLKPCDYPDIKHGGLY 318
                                                                                                                                                                                                                  VSPEKDDVTCVKPHFERFMVKAENDKEKYSVGASVELICRPGFTKMQSTVSVECLSNGTW 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LRKCQKRPCGHPGDTPFGTFTLTGG-NVFEYGVKAVYTCNEGYQLLGEINYREC---DTD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD
                                                                                                                                                                                                                                                                                                          AVCTESGW-RPLPSC------EEKSCDNPYIPNGDYSPLRI-----
                                                                                                                                                                                                                                                                                                                                      LVCTSNKKWSNSFPTCLMLVCESPQIDNGYIDIGLSRRYNHGQSITVKCSDGYNIVGPET 250
                                                                                                                                                                                                                                                                                                                                                                      MHCSDDGFWSKEKPKCVEISCKSPDVING-SPISQKIIYKENERFQYKCNMGYEYSERGD 230
                                                                                                                                                                                                                                                                                                                                                                                                    NVNWDSNEPVCEIQKCIKPPAVEHGDYL----PNQDVYNYGDAITFKCSLSYTLVGSTT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                 --GWTNDIPICEVVKCLPVTAPENGKIVSSAMEPDRE-YHFGQAVRFVCNSGYKIEGDEE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NFPCDRKRCPTPADLLNGAVHIHGGDNALKFGSNISYECNEGYDLIGS-NVRFCILQDTE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENCK--PPHFTEYRVKSNTEKDLYSVGETAELICRPGYVTNTKIITTECLQNGTW--STP 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QEVFYSCEPG-YDLRGAASMRCTPQGDWSPAAPTCEVKSCD
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                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71526 MW;
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                                                                                                                                                                                                                                             ----KHRTGDEITYQCRNGFYPATRGNTAKCTSTGWI
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 349.5; DB Pred. No. 2.2e-23
                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93D8DE35ABF61EB2 CRC64;
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                                                                             2014 AA
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                                                                                                                                                                                                                                                                Q29531
Q29531;
"Primary sequence of an alternatively spliced form of CR1. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee erythrocytes.";
                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT RECEPTOR 1 PRECURSOR (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
PROSITE;
NON_TER
NON_TER
                                                                       SEQUENCE FROM N.A. MEDLINE; 94292799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1500
                                                       Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P.;
                                                                                                                                                             Pan troglodytes (Chimpanzee).
                                                                                                                                                                                                                                                                                                                                                                   1673 DWSPEAPRCTVKSCDDFLGQLPHG-----RVLFPL 1702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1387 NDFEFPVGTSLNYECRPGY--FGKMFSISCLENLVWSSVED--NCRRKSCGPPPE-PFNG 1441
                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1442 MVHINTDT-QFGSTVNYSCNEGFRLIGSPS-TTCLVSGNNVTWDKKAPICEIISCEPPPT 1499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR1.
Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00084; sushi; 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO00436; -. INTERPRO; IPRO00834; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L24920; AAA51438.1;
HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          erythrocytes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                      296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 SDQTYPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KPKCVEIS-CKSPDVINGSPI-SQKIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                     KLPHCSRVCQPPPEILHGEHTP---SHQDNFSPGQEVFYSCEPG-YDLRGAASLHCTPQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -LPSCEEKSCDNPYIPNGDYSPLRIKHR----TGDEITYQCRNGFYPATRGNTAKCTSTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIVRFRCQPGFVMVGSHTVQCQTNGRWGP 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISNGDFYSNNR----ASFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSP 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCS--DD--GFWSKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                      -WIP-APRCTLKPCD--YPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001424; -.
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2014 AA;
                                                                                                                                               Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153:691-700(1994).
                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2014
                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221280 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.2e-22
                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6D6C3A74D81F1DB9 CRC64;
                                                                                                                                                                                                                                                                                    661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2014;
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Q28797
ID Q28797
ID Q2
AC Q2
DT 011
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Best Local :
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                              Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 13, Last sequence update)
01-NAY-2000 (TrEMBLrel. 13, Last annotation updat
UNKNOWN PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q28797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PFAM; PF00084; sushi; 9.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1
                                     INTERPRO; IPR000436; -.
INTERPRO; IPR000834; -.
PFAM; PF00084; sushi; 8.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_1.
                                                                                                                                                                                                                                                       Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P. "Primary sequence of an alternatively spliced form of CR1. Candidate for the 75,000~\text{M}(r) complement receptor expressed on chimpanzee
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 94292799.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q28797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERPRO; IPRO01424; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INTERPRO; IPRO00436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L24921; AAA51439.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Immunol. 153:691-700(1994).
                                                                                                                                                                                                                            erythrocytes.";
                                                                                                                                                   EMBL; L24922; AAA50460.1;
HSSP; P08603; 1HFI.
  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
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                                                                                                                                                                                                         Tummuot
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QEVFYSCEPG-YDLRGAASLRCTPQGDWSPATPTCEVKSCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FVMKGPPRVKCQALNKWEPELPSC-SRVCQPP--PDVLHAERTQRDKDNFSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WDNETPICDRIPCGLPPTI-TNGDFISTNRE---NFHYGSVVTYRCNPGSGGRKVFELVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNAPEWLPFARPINLT - - - - DEFEFPIGTYLNYECRPGYYGRPFSIICLKNSVWTGAKD -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CNE---LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RCRRKSCRNPPDPVNGMVHVI--KDIQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 AA;
  522 AA;
                                                                                                                                                                                                         153:691-700(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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>661
661
72966 M
  57304 MW;
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29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 342.5; DB |
Pred. No. 9.8e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPLEMENT RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
  DB8456EF462C00C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3F0DF1532664D3F0 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
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                                                                                                                                                                                                                                                                                                             Atkinson J.P.;
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Q22328;
01-NOV-1996
01-NOV-1996
                                                                                                                                                                                                                                                                             Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Lightning J., Lloyd C., Rifken L., Roopra A., Saunders D., Shownkeen I
Farsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                      STRAIN-BRISTOL N2;
Geisel C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=BRISTOL N2;
MEDLINE; 94150718.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COSMID T07H6.
 SEQUENCE
              PFAM; PF00084;
                                             EMBL; U53344; AAA96225.1; HSSP; P10998; 1VVC.
                                                                           Submitted (APR-1996)
                                                                                             Waterston R.;
                                                                                                      STRAIN-BRISTOL N2;
                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                         Submitted
                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  Nature 368:32-38(1994).
                                                                                                                                                                                                                                                   elegans.
                                                                                                                                                                                                                                                        "2.2 Mb of contiguous nucleotide
elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                             NTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSRVCQPPPDVLHGERTQRDKDNFSP-----GEEVYYSCEPGY--DLRGSTYLHCTPQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEEKSCDNPYIPNGD-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKC-LPVTAPENGK 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRHVHCQALNKWEPELPS
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95; Conserv
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560 AA; 6
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                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                       EMBL/GenBank/DDBJ
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 FB8923BAC1B320C9 CRC64;
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Best Local Similarity
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              O9YTQ8 PRELIMINARY; PRT; 360 AA.
09YTQ8;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
COMPLEMENT CONTROL PROTEIN HOMOLOG CCPH.
                                                                                                                                                                                                                                                                                      *Albrecht J.-C., Fleckenstein B.;

"Primary Structure of the Herpesvirus Ateles Genome.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.

EMBL; AF083424; AAC95530.1;

EMBL; AF083424; AAC95530.1;
                                                                                                                                                                                                                                                                                                                                                                                                             Ateline herpesvirus 3.
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                 PFAM; PF00084; sushi; 4. SEQUENCE 360 AA; 40208 MW;
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INTERPRO; IPR000436; -.
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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    363 CHNWPPRVPHARI--LFSKSSHGSIAKYECNNGYHPNRNNQIIKCLYGEWTKDGPPMKCL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  243
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249 CDN--PYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWI---PAPRCT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 VEISCK-SPDVING----- 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 CSRPSSPLHGKVVGSSLT-----YQSVVTYSCDHGYRLVGQVQRICLAEGIWGGNEPRC 242
                                                      24 PKRNRYVSLRYVNITN--SSGSYPNGTTLQVTCRKGY--IGRQIQTVTCVNGNWTVPN-- 77
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                                                                                       PRRNTEI -----LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI--MVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCRVPHIQNGKIRDKSEGQLIASGSKVIVECNKQHEANIDERLICSNSTWSHVPVCSPLS 362
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                                                                                                                              103;
                                                                                                                         17.9%; Score 335; DB 12; Length 360; ilarity 33.4%; Pred. No. 2.2e-22; Conservative 32; Mismatches 119; Indels 5
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                                                                                                                                                                                                                                                                   134 NWTPRPPICEITKCKPPPTIANGTHTNI-----KEYYTYLDAVTYSCNDETKLTLTGPSS 188
291 CNQNCTTS 298
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                                             NTAKCTST 294
                                                                                      ETPNMCKNGVWFPALPTCEK-----PAPPRGD-----MPHIDSGEDTST------PSGRN 290
                                                                                                                               RGDAVCTESGWRP-LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRG 286
                                                                                                                                                                            KQCSETGRWVPDEETKCEFKVCKIPQVANGHVEVRKT--SNNVQYQYVNIKCDKGFRLQG 246
                                                                                                                                                                                                                                                                                                                 -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYK--IEGDEE 171
                                                                                                                                                                                                                                                                                                                                                              -ECQKRRCSTPADLLNGWYTVT-GNLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRV 133
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Search completed: November 21, 2000, 16:48:55 Job time: 333 sec

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Maximum DB seq length: 200000000
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1. /SIDSI/gcgda*
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                         /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT:*
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293.168 Million cell updates/sec
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

12	11	10	9	8	7	6	ហ	4	ω	N	1	Result
434	434	437	437	437	437	437	438	481.5	544.5	918	990	Score
17.7	17.7	17.8	17.8	17.8	17.8	17.8	17.8	19.6	22.2	37.4	40.3	% Query Match I
543	496	2317	2039	1930	778	453	543	581	578	216	240	% Query Match Length DB
13	20	10	20	19	19	20	13	12	20	18	18	
R28557	Y55752	P92219	Y55751	W45899	W73147	Y55757	R28547	R13490	Y09065	W39155	W39154	ID
CR1-4 (99H, 103E)	Human CR1 protein	CR1 protein. Homo	Human C3b/C4b rece	Human complememt r	Amino acid sequenc	Human CR1 protein	CR1-4 (52S, 53S, 5	Human C4 binding p	Human complement f	Clone pRRB9FH410 C	Human partial Comp	Description

Treating or screening for cancer, e.g. renal or urogenital cancer - by modulating or detecting tumour associated human complement Factor

WPI; 1997-512742/47. N-PSDB; V02790. Enfield DL, Hass GM,

Kinders RJ;

45	44	43	42	41	40	39	38	37	36	35	34	y y	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
409	412	419	419	420	420	420	421	422	423	423	424	425	425	425	425	426	426	426	427	427	428	428	428	428	428	429	430	431	432	432	434	434
	16.8		٠	17.1	17.1	•	•	•	•	•	•	•	•	17.3	•	17.4	17.4		17.4	•	•	•	17.4	•	•	•	•	•	17.6	•	•	17.7
450	438	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	543	450	2039	543	2039	1537
20	20	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	13	20	12	13	14	12
Y55753	Y55756	R28559	R28543	R28566	R28546	R28544	R28554	R28561	R28564	R28556	R28569	R28568	R28562	R28551	R28549	R28567	R28563	R28555	R28552	R28545	R28571	R28565	R28558	R28553	R28550	R28548	R28560	Y55754	R11810	R28570	R36743	R11982
Human CR1 protein		CR1-4 (114-117STKP	CR1-4 (35E, 37Y) a	72	-4 (44T, 47D,	-4 (35E)	-4 (92T,	-4 (115T)	-4 (116K	-4 (94H) a	-4 (369-	-4 (347T	-4 (116K)	-4 (65T	-4 (64K,	18-3	-4 (117P)	-4 (92T) a	-4 (78T,	-4 (37Y)	-4 (364-3	-4 (1210	09N,	-4 (85R,	$\overline{}$	•	-4 (114S)	pro		CR1-4 (266-274 KLK	sar	Partial human comp

ALIGNMENTS

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W39154;
W39154;

27-APR-1998 (first entry)

Human partial Complement factor H protein fragment 1.

Complement factor H; tumour associated antigen; renal cancer; urogenital cancer; medicament; modulator.

Homo sapiens.

W09738136-A1.
16-OCT-1997; 97WO-US05710.
09-APR-1997; 97US-0812481.
09-APR-1996; 96US-030048.
09-APR-1996; 96US-030048.
06-MAR-1997; 97US-0038614.
(BARD-) BARD DIAGNOSTIC SCI INC.
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RESULT
W39155
ID 9155
ID 925
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09-APR-1996;
09-APR-1996;
           H related antigen, or nucleic acid encoding it
                            Treating or screening for cancer, e.g. renal or urogenital cancer by modulating or detecting tumour associated human complement Fact
                                                                                                                                                                      Enfield DL,
                                                                                                                                                                                                                                                               06-MAR-1997;
                                                                                                                                                                                                                (BARD-) BARD
                                                                                                                                                                                                                                                                                                                                                                         09-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9738136-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    urogenital cancer; medicament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone pRRB9FH410 CFH related protein fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W39155 standard; Protein; 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            such proteins and a CFH antigens can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This partial protein sequence represents a region of the human tumour-associated complement factor H (CFH). This sequence is used in the identification of complement factor H related proteins and antigens isolated from clone prBB9FH410 (see W39155). The detection of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H related antigen, or nucleic acid encoding it
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                                                                                                       V02791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  factor H; tumour associated antigen; renal cancer;
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                                                                                                                                                                    Hass GM,
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                                                                                                                                                                                                                DIAGNOSTIC SCI INC.
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97US-0038614.
                                                                                                                                                                                                                                                                                                       96US-0015083.
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                                                                                                                                                                      Kinders RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21;
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Matches 158;
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Human proteins with secretory signal sequences and nucleotide sequences, useful in control of proliferation and differentian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human complement factor H; immunological mechanism; complement reaction; gene therapy; immune stimulation; haematopoiesis regulation; chemotactic; tissue growth activity; anti-inflammatory; tumour inhibition;
                                                                                                                                                              Kato S,
                                                                                                                                                                                                                                                                                            06-OCT-1997;
                                                                                                                                                                                                                                                                                                                                             02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This partial protein is found in clone pRRB9FH410 and represents a complement factor H related protein with homology to a region of the human tumour-associated complement factor H (CFH). The detection of this protein and a CFH antigen can be used in screening or for the treatment of renal or urogenital cancer, e.g. bladder, cervical or prostate cancer. Agents that may modulate this antigen could be used in the manufacture of a medicament for the treatment of a tumour cell.
                                                                                                                                                                                                               (SAGA ) SAGAMI CHEM RES CENT
                                                                                                                                                                                                                                        (PROT-) PROTEGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secretory signal.
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                                                                                                                                                              Sekine S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            216 AA;
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73.1%;
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  proliferation and differentiation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39;
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Claims 1; Page 55-58; 71pp; English

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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This DNA encodes a protein having homology to human complement factor H, which plays a role in the immunological mechanism involving the complement reaction. The protein can also be used as an antigen for preparing antibodies against the protein. The cDNA can be used as a probe for gene diagnosis and the gene for gene therapy, as well as for large-scale expression of the protein. The protein may also have immune stimulating or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, anti-inflammatory receptor/ligand activity, etc. The protein is identified by the presence of a hydrophobic N-terminal secretory signal region, knowledge of the protein function is not required, as in e.g. methods of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                    Human C4 binding protein.
                                                                                                                                                                                                                                                                                                                                                                                          30-OCT-1991 (first entry)
                                                                                                                                                                                                                        short consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R13490 standard; Protein; 581
                                    Peptide
                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 426 R 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   394 k 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 nfvtpsgsywdyihctqdgwsptvp-----clrtcsksdveiengfi----sesssiyi 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 canggev-----kpcdfpeighgglyykslrrlyfpaaaggsys-----yycdg 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48 CKNGEWVPSNPSRICRKRPCGHP----GDTPFGSFR-----LAVGSEFEFGAKVVYTCDE 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lneetgynckpgyatadgnssgsitclqng-wstq-picikf-cdmpvfensraksngmw 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peiqhghlyyentrrpyfpvatgqsysyycdqnfvtpsgsywdyihctqdgwlptvpclr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLR 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ttsfpqkvylpw-----srveyqcqs-yyelqgskyvtcsngdwsepprcismkpcef
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----fklhdtldyecydgyessygnttdsivcgedgwshlptcynssescgppppisngd 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKPVYKENERFQYKCKQGF--VYKERGDA-VCTGSGWNPQPSC---EEMTCLTPYIPNG- 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGQVVRFECNSGFKI----EGQKEMHCSENGLWSNEKPQCVEISCLPPRVEN-----GDGIY 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYQL-LGEI-DYRECDADGWINDIPICEVVKCLPV----TELENGRIVSGAAEPDQEYY 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QCIFH--YVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQD--TYYCTENGWSPPPKCV 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----IYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRC-SLKPCDF 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136;
                                                                                                                                                                                                                                                  monomer; complement protein; pJOD.C4bp.3; SCR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                     repeat
1..32
/label= signal_peptide
                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.2%; Score 544.5; DB 20; Length 578; 32.3%; Pred. No. 9.1e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147;
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δõ 밁 δÃ

 $\frac{3}{3}$

60 RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDAD----G

2 DCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVC-KNGEWVPSNPS

ncgppptlsfaapmditltetrfktgttlkytclpgyvrshstqtltcnsdgewvynt--

90

Best Local Similarity

Conservative

78; Mismatches

195;

Indels

99;

Gaps

```
This sequence was deduced from human hepatocyte (Hep G2) cDNA obtained following PCR amplification. The protein is a monomer containing 8 SCRs. Each SCR forms a looped domain due to the presence of two intradomain disulphide bonds (only the disulphide bonds of SCR8 are labelled in the Features Table). Within each SCR, the first cysteine residue bonds with the third and the second cysteine residue bonds with the fourth. This secondary structure is responsible for the conformational flexibility of the C4bp monomer. The invention covers fusion proteins in which the monomer sequence, or a specified subfragment of it, e.g. having 5, 4, 3 or 1 SCR(s) is fused to the C-terminal of a protein such as a viral receptor, cell ligand, a bacterial, viral or parasitic immunogen, enzyme, cytokine, toxin, etc. See also Q13243-51.
                                                                                                                                                                                                                                                                         New C4 binding protein fusion proteins and DNA encoding them comprise assemblies of C4bp monomers linked to functional moiety, e.g. AZT, useful as delivery vehicles in diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disulfide-bond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-AUG-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9111461-A.
                                                                                                                                                                                                                                                 Example 1; Fig 1; 105pp; English.
                                                                                                                                                                                                                                                                                                                            N-PSDB; Q13242
                                                                                                                                                                                                                                                                                                                                                                   Pasek MP, Winkler G,
                                                                                                                                                                                                                                                                                                                                                                                           (BIOG-) BIOGEN INC
                                               Sequence
                                                                                                                                                                                                                                                                                                                                          1991-252613/34.
                                                  581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                              91WO-US00567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "intradomain"
65..92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Label
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= C4bp
33..93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "responsible for multimer assembly" 34.80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= SCR3
407..464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    280..345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "intradomain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= SCR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= C4bp_core
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'label= SCR7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    219
19.6%; Score 481.5; DB 1
26.5%; Pred. No. 5.8e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SCR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCR6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SCR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCR5
             DB 12;
             Length 581;
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(UNIW ) UNIV WASHINGTON
                                 03-MAY-1991;
                                                                                                                                                                                /note= "TRUNCATED"
Misc-difference 52
                                                         28-APR-1992;
                                                                                11-NOV-1992
                                                                                                                                           Misc-difference 54
                                                                                                                                                                Misc-difference
                                                                                                                                                                                                                                                                                                                                                           short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                CR1-4 (52S, 53S, 54P) analogue.
                                                                                                                                                                                                                                                     Region
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                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R28547 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           441 gyilvgqa---klscsyshwsapapqckalcrkpelvngrlsvdkdqyvepenvtiqcds 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                498 gygvv-gpqsitcsgnrtwypevpkc 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 GYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  281 YPATRSPVSKCTITG--WIPAPRCSLKPCDFPQFKHGRLYYEESRRP----- 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 AV--C-TGSGWNPQ-PSCEEMTCLT-PYIPNGIYT--PHRIK---HRIDDEIRYECKNGF 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       203 venetigvwrpspptcekitcrkpdvshgemvsgfgpiynykdtivfkcqkgfvl--rgs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         svihcdadskwnpsppacepnscinlpdiphaswetyprptkedvyvvgtvlryrchpgy 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GFTTPSQSYWDYLRCTVNGWEPEVP-CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHS 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fschetsrfsaicqgdgtwsprtpscgdicnfppkiahghykqsssysffkeeiiyecdk 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -EN----GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS 175
                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                               91US-0695514
                                                        92EP-0303826.
                                                                                                                                                                                                                               /label= SCR-8
511..543
                                                                                                                           /note= "Ala substituted by Pro (SCR-8)"
                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                  note= "Gly substituted by Ser (SCR-8)"
                                                                                                                                                                           note= "Thr substituted by Ser
                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                /label= SCR-2
                                                                                                                                                                                                                                                                                       /label= SCR-1
                                                                                                                                                                                                                                                     .510
                                                                                                                                                                                                                 SCR-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YFPVPIG----
                                                                                                                                                                            (SCR-8)"
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RESULT
Y55757
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 133;
22-FEB-2000 (first entry)
                                                 Y55757;
                                                                                          Y55757 standard; Protein; 453 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                specified substitution variants of it are claimed in which certain positions in SCR-1 which have been identified as important for the degree of C3b- and C4b-binding are substituted by amino acids from the corresponding positions in SCR-8. The specification does not contain the CRI-4 sequence; the sequence given here was constructed from the full-length CRI amino acid sequence having GENESEQ accession number RI1810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The CDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of them.
                                                                                                                                                                                               391 htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 11; Fig 2 and R11810; 23pp; English
                                                                                                                                                                                                                                                                                                                                                                               309 aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy-- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                            359 ---cvlagmeslwnssvpvceq-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for diagnosis etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1992-375009/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Atkinson JP,
                                                                                                                                                                                                                                                                                                                                       353 YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                              299 APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwspa 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      245 EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 kctppnvengilvsdn---rslfslnevvefrcqpvfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81 qfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfis 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EFGAKVYYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141 : | : | : | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gtylnyecrpgysgrpfsiiclknsvw--sspkdrcrrkscrnppdpvngmvhvikg--i 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               543 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17.8%; Score 438; DB 13; 27.9%; Pred. No. 1.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krych M;
                                                                                                                                                                                                                                                 ------GQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               148;
                                                                                                                                                                                                                                                                                         ----ifcpsppvipngr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 132;
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31;

Human CR1 protein LHR-C fragment.

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Best Local Similarity
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24-FEB-1993;
01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                   may be mediated through the inhibition of complement pathway enzymes. The soluble CRI protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CRI protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmene disorders. CRI proteins, analogues, derivatives, and anti-CRI antibodies are used in assays, and diagnostics. The present sequence represents the human CRI protein long homologous repeat (LHR)-C fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C3B/C4B receptor; CRI protein; cell-surface protein; erythrocyte; human; complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; long homologous repeat; LHR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a human C3B/C4B receptor (CR1) protein. The CR1 protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 5B; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cardiant activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A human C3B/C4B receptor (CR1) protein having antiinflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-633357/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marsh
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(AVAN-) AVANT IMMUNOTHERAPEUTICS 1
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                                                                                                                                                                                                                                                                                 27
                                                                                                                                        GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                       qvgsrinyscttghrligh-ssaecilsgntahwstkppicqripcglppt-iangdfis 139
                                                                                                                                                                                                            EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                                                              gtslkyecrpeyygrpfsitcldnlvw--sspkdvckrkscktppdpvng--mvhvitdi 81
                                                                                                                                                                                                                                                                                 GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                  kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc
                                                                     SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                    tnre---nfhygsvvtyrcnlgsrgrkvfelvgepsiyctsnddqvgiwsgpapqciipn 196
EEMTCLTPYIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIP-APR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carson GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong WW,
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74US-0350238.
93US-0026134.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88US-0176532
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                                                                                                                                                                                                                                                                                                                                  17.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Makrides SC, Klickstein LB,
                                                                                                                                                                                                                                                                                                                  64;
                                                                                                                                                                                                                                                                                                                                    Score 437; DB 2
Pred. No. 1e-25;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INC.
                                                                                                                                                                                                                                                                                                                                                      DB 20;
                                                                                                                                                                                                                                                                                                                     161;
                                                                                                                                                                                                                                                                                                                                                      Length 453;
                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                     98;
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                                                                                                                                                                                                                                                                                                                     Gaps
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W73147 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        autoimmune response; neurological response; Alzheimer's disease; parkinson's disease; multiple sclerosis; systemic lupus erythematosus; rheumatoid arthritis; myasthenia gravis; epidermis bullosa;
                                                      an interferon-gamma secretory response, autoimmune response or neurological response, e.g. Alzheimer's or Parkinson's disease or multiple sclerosis. Also the protein can be used to treat systemic lupus erythematosus, rheumatoid arthritis, myasthenia gravis,
                                                                                                                                                                     B-cell-mediated immune response to prevent immune response-mediated tissue rejection and destruction or clearance or inactivation of an expressed protein especially from cells that have been treated by gene
                                                                                                                                                                                                                               receptor 1 (SCR1), useful in the treatment of T-cell or B-cell mediated immune responses. It is used to inhibit a T-cell or
                                                                                                                                                                                                                                                  This is an amino acid sequence of the human soluble complement receptor 1 (sCR1), useful in the treatment of T-cell or B-cell
                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 54pp; English.
                                                                                                                                                                                                                                                                                                                                              Fragment of soluble human complement receptor 1 - useful for treating T-cell or B-cell mediated immune responses e.g. inflammatory responses such as rheumatoid arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1998-568350/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Annenkov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9845430-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hashimoto's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dystrophin; inflammatory response; interferon-gamma secretory response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of the soluble complement receptor 1 (sCR1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               409
                                                                                                                                 therapy to express the protein, e.g. dystrophin. The protein can also be used to inhibit a T-cell or B-cell-mediated inflammatory response,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ANNE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             254 srvcqpppeilhgehtpshqdnfspgqevfyscepg-ydlrgaaslhctpqgdwspeapr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       362 lvghrslwnnsvpvceh-ifcpnppailngrhtgtpsgdipygeisny------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNG----WEPEVPCLRQCIF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QC--HSGYSLP---NGQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cavkscddflgqlphgrv-----lfplnlqlgakvsfvcdegfrlkgss---vshcv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSLKPCD--FPQFKHGRLYYEESRRPYFP--VPIGKEYSYYCDNGFTTPSQSYWDYLRCT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tcdphpdrgmtfnligestirctsdphgngvwsspaprc 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       soluble complement receptor 1; sCR1; T-cell; B-cell; ed immune response; inhibition; tissue rejection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANNENKOV A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHERNAJOVSKY Y.
                                      bullosa or Hashimoto's disease.
    778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chernajovsky Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97GB-0006950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98WO-GB01012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----HY----VEYGESSYWQRRYIEGQSAKV 396
                                                                                                                                                     The protein can also
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Sequence

Query Match

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             Derivatives of soluble poly:peptide(s) bonded to low affinity
                                                                                       WPI; 1998-110524/10.
                                                                                                                                                     Dodd I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Membrane binding element; thrombotic disease; soluble protein; complement-related disease; integral membrane protein; inflamm short consensus repeat; SCR 1-3; CRI; complement receptor type
                                                                                                                                                                                                                                                                                          15-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                        08-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cross-links
                                                                                                                                                                                                                    (ADPR-) ADPROTECH PLC
                                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9802454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human complement receptor 1 (residues 1-1929).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W45899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W45899 standard; peptide; 1930 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      437 htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        355 aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy-- 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299 srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpggdwspa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 GAAEPDQEYYFGQYVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127 qfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfis 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71 gtylnyecrpgysgrpfsiiclknsvwtgakdr--crrkscrnppdpvngmvhvikg--i 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---cvlagmeslwnssvpvceq-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                                                                     Mossakowska DEI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                      96GB-0014871
                                                                                                                                                                                                                                                                                                                                                     97WO-EP03715.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Disulphide linked to Cys in peptide given
in W45889"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17.8%; Score 437; DB 19; 27.7%; Pred. No. 2.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---ifcpsppvipngr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31;
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Y55751
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; human;
                                          Human C3b/C4b receptor (CR1) protein.
                                                                                            22-FEB-2000 (first entry)
                                                                                                                                                                                    Y55751 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immuno-modulators for treating multiple sclerosis. (A) are administered orally, topically, by injection or inhalation at 0.01-10 (preferably 0.1-10) mg/kg/day.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents human complement receptor 1 (CR1, CD 35) N-terminal fragment. The invention relates to a soluble derivative (A) of a soluble polypeptide (I), which comprises at least 2 heterologous membrane-binding elements (MBE) of low membrane affinity covalently associated with (I). MBE interact, independently and with thermodynamic additivity, with components of cellular or artificial membranes exposed to extracellular fluids. (A) are used to treat disorders treatable with (I) itself, specifically inflammation or any other complement-related disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorder (e.g. neurological disease, graft rejection, myocardial infarction, sepsis, rheumatoid arthritis and many others; including application to indwelling devices) and thrombolytic disease, but also treat allergy, induce weight loss, to treat ischaemia or astuma and as
                                                                                                                                                                                                                                                                                         391 htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 446
                                                                                                                                                                                                                                                                                                                                                                                        359 ---cvlagmeslwnssvpvceq--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              253 srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwspa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 22; Pages 60-61; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           membrane binding groups - useful for treating complement-related and thrombotic diseases, providing improved localisation at cellular
                                                                                                                                                                                                                                                                                                                                                                                                                              353 YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           139 tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81 qfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfis 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP- 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gtylnyecrpgysgrpfsiiclknsvwtgakdr--crrkscrnppdpvngmvhvikg--i 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1930 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                      2039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches 149;
                                                                                                                                                                                                                                                                                                                      -GQDTYYCTE----NG-W-SPPPKC 424
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Best Local
                                                                                                                                                                                                                                                                                                                                                      Matches 132;
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06-DEC-1974;
24-FEB-1993;
01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      length human CR1 as expressed on erythrocytes. The CR1 function in vivo may be mediated through the inhibition of complement pathway enzymes. The soluble CR1 protein exhibits a complement regulatory activity, and this may be used to prevent reperfusion injury, inhibit Arthus reaction, and neutrophil mediated tissue damage, and reduce myocardial infarct size, and inflammation. The CR1 protein and its fragments can also be used in the treatment of conditions which involve unwanted complement activity, e.g. shock lung, tissue damage due to burn, or ischemic heart conditions, and autoimmune disorders. CR1 proteins, analogues, derivatives, and anti-
CR1 antibodies are used in assays, and diagnostics. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; diagnostic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a human C3B/C4B receptor (CR1) protein. The CR1 protein or fragment is expressed as a cell-surface protein on the surface of a non-human cell and exhibits a complement regulatory activity of full
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cardiant activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A human C3B/C4B receptor (CR1) protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-633357/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Concino MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1A-P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; Z38150.
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(BGHM ) BRIGHAM & WOMENS HOSPITAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents the human CR1 protein.
                                                                                                                                                                                                              122
 294
                                 245
                                                                    237
                                                                                                     191
                                                                                                                                        180
                                                                                                                                                                       142 GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                   27
                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                             gtylnyecrpgysgrpfsiiclknsvwtgakdr--crrkscrnppdpvngmvhvikg--i 121
                                                                                                                                                                                                                                                                                                                   GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                                                                                                                                                           EFGAKVVYTCDEGYQLLGEIDYRECDADG----WINDIPICEVVKC-LPVTELENGRIVS 141
srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwspa
                                 EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
                                                                kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc
                                                                                                   SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                        tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn
                                                                                                                                                                                                        qfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carson GR;
                                                                                                                                                                                                                                                                                                                                                                                                                                           2039 AA;
                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0332865.
74US-0350238.
93US-0026134.
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                                                                                                                                                                                                                                                                                                                                                                 17.8%;
27.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Makrides SC,
                                                                                                                                                                                                                                                                                                                                                   ; Score 437; DB 20;
; Pred. No. 6.9e-25;
63; Mismatches 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                having antiinflammatory and
                                                                                                                                                                                                                                                                                                                                                                                      Length 2039;
                                                                                                                                                                                                                                                                                                                                                     Indels 132;
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                                                                                                                                          236
                                                                                                                                                                                                              179
                                                                      293
                                    298
                                                                                                         244
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Ωy

27 GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86

Query Match
Best Local Similarity
Matches 132; Conserv

Conservative

63;

Score 437; DB Pred. No. 8.2e 63; Mismatches

DB 10; 3.2e-25; nes 149;

Length 2317;

Indels 132;

Gaps

31;

17.8%;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                 This is full-length CR1 protein, and shortened forms are new, lacking the transmembrane region. The proteins and fragments bind C3b and/or C4b, have cofactor activity and inhibit C3 and C5 convertase activity. In the sequence, x=untranslated region. This has 7 short consensus repeats (CR) of 4 long direct homologous repeats (LHR) (see fig. 10 in patent). Deletion mutants, eg LHR-A for binding of C4b, and LHR-C for C3b binding, be made, and LHR-B and -C can detect CR2 sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CR1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-FEB-1990
                                                                                                                                                                                                                                                                                               (TCEL ) T CELL SCIENCES INC.
(UYJO ) THE JOHNS HOPKINS UNIVERSITY
(BRIG ) THE BRIGHAM AND WOMEN'S HOSP
                                                                                                                                                                                                                                                                                                                                                    01-APR-1988;
                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                        05-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                  WO8909220-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Complement; cofactor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P92219 standard;
                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                 WPI; 1989-309498/42
 Sequence
                                                                                                                                                                                              New nucleic acid sequences encoding new CR1 protein - and its fragment, for diagnosis and control of complement-related immune defects,
                                                                                                                                                                                                                                     N-PSDB; N91477.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         299
                                                                                                                                                                                   inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        \verb|htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpqgngvwsspaprc|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---cvlagmeslwnssvpvceq---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy-- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                          DT, Klickstein LB,
                                                                                                                                                         Fig 1; 191pp; English.
                         injury.
  2317 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                   myocardial infarct,
                                                                                                                                                                                                                                                                                                                                                      88US-0176532
                                                                                                                                                                                                                                                                                                                                                                              89WO-US01358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 2317
                                                                                                                                                                                                                                                                          Wong W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                   HOSPITAL.
                                                                                                                                                                                   etc
                                                                                                                                                                                                                                                                           Carson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                           Concino MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ifcpsppvipngr 431
                                                                                                                                                                                                                                                                           Makrides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             487
                                        prevent
                                                                                                                                                                                                                                                                            SC;
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Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
Y55752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Дb
                          A human C3B/C4B receptor (CR1) protein having antiinflammatory and
                    cardiant activity
                                                            WPI; 1999-633357/54
                                                                                                    Concino MF,
                                                                                                                                                                                                                                                                                                                                                                          complement regulatory activity; complement pathway enzyme; tissue damage; reperfusion injury; Arthus reaction; myocardial infarct; inflammation; heart condition; autoimmune disorder; long homologous repeat; LHR; SCR;
                                                                                                                                               (UYJO ) UNIV JOHNS HOPKINS
(BGHM ) BRIGHAM & WOMENS H
                                                                                                                                                                                      01-APR-1988;
                                                                                                                                                                                                     24-FEB-1993;
                                                                                                                                                                                                                               03-APR-1989;
                                                                                                                                                                                                                                                          06-JUN-1995;
                                                                                                                                                                                                                                                                                    09-NOV-1999
                                                                                                                                                                                                                                                                                                              US5981481-A.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    C3B/C4B receptor; CR1 protein; cell-surface protein; erythrocyte; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human CR1 protein LHR-A SCR fragment.
                                                                                                                                                                                                                06-DEC-1974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y55752 standard; Protein; 496 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                441 htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131 qfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfis 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---cvlagmeslwnssvpvceq----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwspa 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EFGAKVVYTCDEGYOLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                                                                                                                                                                                   consensus repeat.
                                                                                                                                            BRIGHAM & WOMENS
                                                                                      Carson
                                                                                      Wong WW,
arson GR;
                                                                                                                              IMMUNOTHERAPEUTICS INC.
                                                                                                                                                                                                  89US-0332865.
74US-0350238.
93US-0026134.
                                                                                                                                                                                     88US-0176532.
                                                                                                                                                                                                                                                         95US-0470652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Makrides SC,
                                                                                                                                              HOSPITAL.
                                                                                                 Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --ifcpsppvipngr
                                                                                                  Fearon
                                                                                                  DT,
                                                                                                 Ę
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Matches 133;
437 grhtgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 494
                                                           407
                                                                                                             407
                                                                                                                                                           351
                                                                                                                                                                                                             355
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                                                                                                                                                                                                                                                                                                                                                           244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27 GTQATYKCRPGYRTLGTIVKVC-KNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                 WDYLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciip 241
                                                                                                       ----cvlagmeslwnssvpvceq----
                                                                                                                                                                                                aaptcevkscddfmgqqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy
                                                                                                                                                                                                                                                                                                csrv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwsp
                                                                                                                                                                                                                                                                                                                                                    CEEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP 298
                                                                                                                                                                                                                                                                                                                                                                                                     nkctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iqfgsqikysctkgyrligs-ssatciisgdtviwdnetpicdripcglppt-itngdfi 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gtylnyecrpgysgrpfsiicclknsvwtgakdr--crrkscrnppdpvngmvhvikg-- 126
                                                                                                                                                                                                                                                    -APRCSLKPCD---FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSY 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.7%;
27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 148; Indels 134;
                                                   -GQDTYYCTE----NG-W-SPPPKC 424
                                                                                             --ifcpsppvipn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     298
                                                                                                                                                                                                                                                                                                                                                                                                                                                      243
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RESULT 12
R28557
ID R28557 standard; peptide; 543 AA.

XX
AC R28557;
XX
DT 19-MAR-1993 (first entry)
XX
DE CR1-4 (99H, 103E) analogue.
XX
XX
KW short consensus repeat; regulator of complement activation;
XX
KW C3b binding; C4b binding; human complement type 1 receptor.
XX
OS Homo sapiens.
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                                          Вb
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                                                                                                 밁
                                                                                                                       QY
                                                                                                                                                     В
                                                                                                                                                                              δÃ
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                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                           The cDNA clone designated CR1-4 was described in J.Exp.Med.(1988) 168:1255-1270. It encodes the first 8 and a half amino terminal SCRs of CR1. The invention concerns analogues of "regulator of complement activation" proteins or truncated, hybrid or recombinant forms of them. CR1-4 is a preferred truncated form and a number of specified substitution variants of it are claimed in which certain positions in SCR-2 which have been identified as important for the degree of C3b and C4b-binding are substituted by amino acids from the corresponding positions in SCR-9. The specification does not contain the CR1-4 sequence; the sequence given here was constructed from the full-length CR1 amino acid sequence having GENESEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement activity regulator protein analogues - useful for treating auto: immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAY-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Atkinson JP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP512733-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                  accession number R11810 and descriptions in the disclosure
                                             196
                                                                                                  139
                                                                                                                            142
                                                                       191
                 245
                                                                                                                                                                                 87
                                                                                                                                                       81
                                                                                                                                                                                                            25
                                                                                                                                                                                                                                        27
                                          kctppnvengilvsdn---rslfslnevvefrcqpvfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                     GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
thre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn 195
                                                                                                                           GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                  EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                           gtylnyecrpgysgrpfsiiclknsvwtgakdr--crrkscrnppdpvngmvhvikg--i 80
                                                                     SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                    132;
                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fig 2 and R11810; 23pp; English.
                                                                                                                                                                                                                                                                                                                                        543 AA;
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hourcade D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91US-0695514.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92EP-0303826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= SCR-8
511..543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Thr substituted by Glu (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "TRUNCATED"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= SCR-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= SCR-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Ser substituted by His (SCR-9)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .510
                                                                                                                                                                                                                                                                                 17.7%;
27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCR-9
                                                                                                                                                                                                                                                                    63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krych
                                                                                                                                                                                                                                                                                 Score 434; DB 13;
Pred. No. 2.2e-25;
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X
                                                                                                                                                                                                                                                                     149;
                                                                                                                                                                                                                                                                                               Length 543;
                                                                                                                                                                                                                                                                     Indels 132;
                                                                                                                                                                                                                                                                  Gaps
                  298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QΥ
  Вþ
                                                                                                                                                                                         (TCEL-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R11982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R11982 standard;
This sequence comprises three of the four tandem, direct, long homologous repeats of the full-length F allozyme of CR1. LHR-A absent. Each LHR might represent a single C3b/C4b binding doma.
                                                                Human complement receptor type 1 gene, encoded proteins and fragments - for treatment of immune disorders, myocardial idemage due to inflammmation and in treatment of thrombosis
                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partial human complement type 1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-JUN-1991
                                                                                                             N-PSDB; Q11643.
                                                                                                                        WPI; 1991-132854/18.
                                                                                                                                                                                                                           26-SEP-1990;
                                                                                                                                                                                                                                       26-SEP-1989;
                                                                                                                                                                                                                                                             25-SEP-1990;
                                                                                                                                                                                                                                                                                  18-APR-1991.
                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ımmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement system; C3b/C4b receptor; CR1; allergic reaction;
                                            Disclosure; Fig 5; 234pp; English.
                                                                                                                                                           Fearon DT,
                                                                                                                                                                              (BRIG-) BRIGHAM AND WOMEN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391 htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253 srv-cqpp--pdvlhaertqrdkdnfspgqevfyscepg-ydlrgaasmrctpqgdwspa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---cvlagmeslwnssvpvceq---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aptcevkscddfmgqllngrv--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       response; long homologous repeat; LHR.
                                                                                                                                                                                                    T CELL SCI INC
                                                                                                                                                                                          JOHNS HOPKINS UNIVERSITY.
                                                                                                                                               sc,
                                                                                                                                                           Klickstein LB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                              Marsh
                                                                                                                                                                                                                           89US-0412745.
90US-0912349.
                                                                                                                                                                                                                                                            90WO-US05454
                                                                                                                                                                                                                                                                                                                                                          /note= "positively-charged; preceded by hydrophobic
sequence"
1521..1526
                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= LHR-B
439..891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein; 1537
                                                                                                                                                                                                                                                                                                                                                                                                                                /label= LHR-C
                                                                                                                                                                                                                                                                                                                              "has 67 per cent homology kinase C phosphorylation receptor"
                                                                                                                                                         Wong WW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----lfpvnlqlgakvdfvcdegfqlkgssasy--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---GQDTYYCTE----NG-W-SPPPKC
                                                                                                                                                           Carson GR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----ifcpsppvipngr
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the F
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   domain
                                                                              infarct,
                                                                                                                                                            Concino MF;
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              is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                 C3b/C4b receptor; CR1; erythrocyte; monocyte; macrophage; granulocyte; 1C3b; T cell; splenic follicular dendritic cell; soluble; complement; glomerular podocyte; B cell; C3b; C4b; inactivated C3b; phagocytotsis; plasma; ligand binding activity; immune complex; activator; allotype; endocytosis; lymphocyte; classical; alternative; pathway; cofactor; F; C3/C5 convertase; liver; cleavage; factor I; regulation; glycoprotein;
                                 Protein
                                                                    Peptide
                                                                                                                                                         endoglycosidase
                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                           R36743;
                                                                                                                                                                                                                                                                                                                                                                                                                         R36743 standard; Protein; 2039 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       making the receptor multivalent. The LHR's are composed of 7 short consensus repeats of 60-70 residues resembling the SCR's of other C3/C4 binding proteins. The protein and fragments of it having C3b and/or C4b binding activity can be used to treat immune disorders involving inappropriate complement activity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               See also Q11642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pdrgmtfnligestirctsdphgngvwsspaprc 885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGYSLP----NGQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lvgmrslwnnsvpvceh-ifcpnppailngrhtgtpsgdipy-----gkeisytcdph 851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VNG----WEPEVPCLRQCIF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cavkscddflgqlphgrv-----lfplnlqlgakvsfvcdegfrlkgss---vshcv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CSLKPCD--FPQFKHGRLYYEESRRPYFP--VPIGKEYSYYCDNGFTTPSQSYWDYLRCT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        srvcqpppeilhgehtpshqdnfspgqevfyscepg-ydlrgaaslhctprgdwspeapr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEMTCLTPYIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIP-APR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tnre---nfhygsvvtyrcnlgsrgrkvfelvgepsiyctsnddqvgiwsgpapqciipn 634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gtslkyecrpeyygrpfsitcldnlvw--sspkdvckrkscktppdpvng--mvhvitdi 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        qvgsrinyscttghrligh-ssaecilsgntahwstkppicqripcglppt-iangdfis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                    B; glycosylation; duplication; repetitive intervening sequence;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                     (first entry)
                               /note= "Signal peptide"
503..2039
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.7%;
29.7%;
            "CR1 encoded by CR1 cDNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 64; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 434; DB 12;
Pred. No. 8.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----HY-VEYGESSYWQRRYIEGQSAKVQC--H 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1537;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
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Ъ Qy

966 gtslkyecrpeyygrpfsitcldnlvw--sspkdvckrkscktppdpvng--mvhvitdi 1021

27 GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF

Matches

Conservative

64;

Mismatches

167;

Gaps

32

Query Match Best Local Similarity

17.7%; Score 434; DB 14; 29.7%; Pred. No. 1.2e-24;

Length 2039;

Sequence

2039 AA;

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internalises bound complexes, either by adsorptive endocytosis

or by phagocytotsis. The function of CR1 on B lymphocytes is less

cwell defined. CR1 can inhibit the classical and alternative pathway

c3/c5 convertases and act as a cofactor for the cleavage of C3b and

c4b by factor I, therefore CR1 has a complement regulatory function

as well as acting as a receptor. CR1 is a glycoprotein composed of

dentified, differing by increments of approx. 40-50 kD. The two most

common forms, the F and S allotypes, also termed A and B allotypes,

have molecular weights of 250 and 290 kD respectively. The two rarer

forms have molecular weights of 210 and 290 kD. These differences

cepresent differences in the polypeptide chain of CR1, rather than

glycosylation state because they are not abolished by treatment of

purified receptor portein with endoglycosidase F. The CR1 gene has
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carson GR, co
                                                                                                                                                                                                                                                                                                                           activators. The consequences of these interactions depends on the type of bearing the receptor. Erythrocyte CR1 binds immune complexes for transport to the liver. CR1 on neutrophils and monocytes
                                                                                                                                                                                                                                                                                                                                                                                                     receptor (CR1). CR1 is present on erythrocytes, monocytes/macro-phages, granulocytes, B cells, some T cells, splenic follicular dendritic cells and glomerular podocytes. CR1 specifically binds C3b, C4b and inactivated C3b (iC3b). A soluble form of the recepis found in plasma which has ligand binding activity and the same molecular weight as membrane-associated CR1. CR1 binds C3b and C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid encoding polypeptide having complement regulatory activity - used to prevent reperfusion injury, inhibit Arthus reaction and neutrophil mediated tissue damage and reduce
                               been shown to have repetitive intervening sequences which may have been duplicated in the formation of the larger allotypes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Fig 1; 90pp; English.
                                                                                                                                                                                                                                                                                                                                                                                   that have covalently attached to immune complexes and other complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the entire amino acid sequence of the C3b/C4b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                myocardial infarct size and inflammation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-APR-1988;
03-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Concino MF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                89US-0332865
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           491..1393
/note= "Long homologous repeat-B"
1394..1843
/note= "Long homologous repeat-C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    161..162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503..490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Unclear in specification"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Long homologous repeat-A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fearon DT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                        tes. CRI specifically binds
A soluble form of the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klickstein LB;
                                                                                                                                                                                                                                                                                                                                                                                                       CR1 binds C3b and C4b
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RESULT 15
R28570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               В
1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1022
                                                                                                                                                                                                                                                                                                                                                                                                              short consensus repeat; regulator of complement activation; C3b binding; C4b binding; human complement type 1 receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CR1-4 (266-274 KLKTQTNASD) analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R28570 standard; peptide; 543 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1354 pdrgmtfnligestirctsdphgngvwsspaprc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1302 lvgmrslwnnsvpvceh-ifcpnppailngrhtgtpsgdipy-----gkeisytcdph 1353
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           WPI; 1992-375009/46
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                                     Atkinson JP,
                                                                                         03-MAY-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kctppnvengilvsdn---rslfslnevvefrcqpgfvmkgprrvkcqalnkwepelpsc 1193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tnre---nfhygsvvtyrcnlgsrgrkvfelvgepsiyctsnddqvgiwsgpapqciipn 1136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEMTCLTPYIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIP-APR 301
                                                                WASHINGTON
                                     Hourcade D,
                                                                                         91US-0695514
                                                                                                                    92EP-0303826
                                                                                                                                                                                                                         /label= SCR-9
/note= "TRUNCATED"
266..274
                                                                                                                                                                                                                                                                                             /label= SCR-2
451..510
                                                                                                                                                                                                                                                                                                                       /label= SCR-1
61..122
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                                                                                                                                                                                                                                                                               /label= SCR-8
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                                                                                                                                                                                                 from SCR-8-9 to increase C3b binding"
                                       Krych
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Complement activity regulator protein analogues - useful for treating auto:immune diseases, to suppress transplant rejection,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid sequence having GENESEQ accession number R11810 and descriptions in the disclosure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 8; Page 18 and R11810; 23pp; English
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    391
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                                                                                                                                                                       aptcevkscddfmgqllngrv-----lfpvnlqlgakvdfvcdegfqlkgssasy--
                                                                                                                                                                                                                                                                                                                                                                                     SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                  tnre---nfhygsvvtyrcnpgsggrkvfelvgepsiyctsnddqvgiwsgpapqciipn 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gtylnyecrpgysgrpfsiiclknsvwtgakdr--crrkscrnppdpvngmvhvikg--i 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF
                                                                                                                                YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                             srv-cqpp--pdvlhaklktqtnsdfspgqevfyscepg-ydlrgaasmrctpqgdwspa
                                                                                                                                                                                                                                                                                                                                                   kctppnvengilvsdn---rslfslnevvefrcqpvfvmkgprrvkcqalnkwepelpsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFGAKVYYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS
                                                                                                                                                                                                                  APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
                                                                                                                                                                                                                                                                                                        EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
htgkplevfpfgkavnytcdphpdrgtsfdligestirctsdpggngvwsspaprc 446
                                                                                        ---cvlagmeslwnssvpvceq----
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                                             -GQDTYYCTE----NG-W-SPPPKC 424
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31;

Search completed: November 21, 2000, 16:43:54 Job time: 293 sec

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Result
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                 409
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Copyright (c) 1993 - 2000 Comp
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JC5194		362		294.5	40
I53821		768		296	39
B72152		263		296.5	38
T28450		263		297.5	37
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S01896		384		298.5	35
I54479		377		298.5	34
A30359		830		309.5	33
137278		270		310	32
A42755		768		310.5	31
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F:146-205/Domain: complement factor H repeat homology <FH03>
F:210-262/Domain: complement factor H repeat homology <FH04>
F:246-248/Region: cell attachment (R-G-D) motif
F:267-320/Domain: complement factor H repeat homology <FH05>
F:325-385/Domain: complement factor H repeat homology <FH06>
                                                                                                                                                                                                                                                                                                                           A;Map position: 1
C;Superfamily: complement factor H; complement factor H repeat homology C;Superfamily: complement alternate pathway; duplication; glycoprotein; plate; complement alternate pathway; duplication; glycoprotein; plate; 1-18/Domain: signal sequence #status predicted <MPT>
F;11-1234/Product: complement factor H #status predicted <MPT>
F;21-180/Domain: complement factor H repeat homology <FH012>
F;85-141/Domain: complement factor H repeat homology <FH012>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926 C;Comment: Two codominant alleles of factor H are present in mice. C:Comment: Factor H functions as a cofactor in the inactivation of C3b by serine prot (C5 convertase) in the alternative complement pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729 R;Munoz-Canoves, P.; Tack, B.F.; Vik, D.P. Biochemistry 28, 9891-9897, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M12660; NID:g193724; PIDN:AAA37759.1; PID:g387181 F:Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y. J. Immunol. 144, 358-362, 1990 A;Title: Demonstration of an unusual allelic variation of mouse factor H A;Reference number: I49711; MUID:90111033 A;Accession: I49711
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A;Title: Murine protein H is comprised of 20 repeating units,
A;Reference number: A26154; MUID:86233353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Mus musculus (nouse mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: A26154; I49711; I49728
R;Kristensen, T.; Tack, B.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
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A;Accession: I49728
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A; Residues: 1-18 < RES>
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A; Residues: 1-1234 < KRI>
                                                                                  F;389-442/Domain:
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A; Residues: 1-19 < RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Analysis of complement factor H mRNA expression:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                      complement factor H repeat homology <PH05>
complement factor H repeat homology <PH06>
complement factor H repeat homology <PH07>
complement factor H repeat homology <PH08>
repeat
    <FH09>
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A:Note: 402-Tyr was also found
A:Note: parts of this sequence, including the amino and carboxyl ends of the mature prof
R:Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
Eur. J. Immunol. 21, 799-802, 1991
A:Title: Human complement factor H: two factor H proteins are derived from alternativel.
A:Reference number: A60238; MUID:91184292
                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S00254; A60238; A54726; A61565; A26505; I72654; S66298
R;Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B.
Biochem. J. 249, 593-602, 1988
A;Title: The complete amino acid sequence of human complement factor H.
A;Reference number: S00254; MUID:88134059
A;Accession: S00254
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F;629-683/Domain: complement factor H repeat homology <FH11>
F;629-683/Domain: complement factor H repeat homology <FH12>
F;690-743/Domain: complement factor H repeat homology <FH13>
F;752-802/Domain: complement factor H repeat homology <FH15>
F;752-802/Domain: complement factor H repeat homology <FH15>
F;808-861/Domain: complement factor H repeat homology <FH15>
F;936-989/Domain: complement factor H repeat homology <FH17>
F;936-989/Domain: complement factor H repeat homology <FH18>
F;936-989/Domain: complement factor H repeat homology <FH18>
F;1053-1107/Domain: complement factor H repeat homology <FH19>
F;1114-1168/Domain: complement factor H repeat homology <FH19>
F;11172-1233/Domain: complement factor H repeat homology <FH19>
F;11172-1233/Domain: complement factor H repeat homology <FH19>
F;1172-1233/Domain: complement factor H repeat h
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                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-1231 <RIP>
A;Cross-references: EMBL:Y00716; NID:g31964; PIDN:CAA68704.1; PID:g31965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPKCIRIK 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPSGYSWDYLRCTAQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QPFCEEKRCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTGWIPVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ICRKKPCGHPGDTPFGSFRLAVGSQFEFGAKVVYTCDDGYQLLGEIDYRECGADGWINDI 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    factor H precursor, long splice form - human
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82.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GDB:120041; OMIM:134370
A;Map position: 1q32-1q32
C;Genetics: <HF2>
                                                                                                                                         A; Note: the C; Function:
                                                                                                                                                                                                                                                                A; Gene: GDB: HF2; HF
A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Comment: Factor H has also been found bound to cell membranes in an unknown manner. C; Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon, D.L.; Bu
Biochim. Biophys. Acta 1289, 305-311, 1996
A;Title: Ractor H co-purifies with thrombospondin isolated from platelet secretate.
A;Reference number: S66298; MUID:96205365
                                                A; Description: a cofactor in the inactivation of C3b by serine proteinase I; also inche alternative complement pathway
                                                                                                                                                                                                                        A; Map position: 1q32-1q32
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A; Residues: 411-419; 574-578, 580-582 < CAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767
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                                                                                                                                                                                 the correspondence between the two loci and the sequences indicated is unclea
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complement alternate

GDB:129095

<HF1>

Gordon, D.L.; Burn

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R;Sim, R.B.; Discipio, R.G.
Blochem. J. 205, 285-293, 1982
A;Title: Purification and structural studies on the complement-system control protein
A;Reference number: A26505; MUID:83048213
A;Accession: A26505
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A; Note: parts of this sequence were determined by Campbell, R.D.; Sim,
                                                                                                                                                                                                 A;Contents: annotation; NMR structure determination, residues 927-985 R;Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.; Weiss, E.H. J. Immunol. 146, 3190-3196, 1991
                                                                                                                                                                                                                                                                                                                     R:NOrman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D. J. Mol. Biol. 219, 717-725, 1991
A;Title: Three-dimensional structure of a complement control protein module in soluti A;Reference number: A49224; MUID:91278097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Solution structure of the fifth repeat of factor H: A second example of A; Reference number: A44551; MUID: 92232649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.; Pearce, J.; Driscoll, Biochemistry 31, 3626-3634, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A61565; MUID:86188123 A;Accession: A61565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R; Ripoche, J.; Day, A.J.; W
Biosci. Rep. 6, 65-72, 1986
A; Status: translated from GB/EMBL/DDBJ
                                  A; Accession: 172654
                                                                                 A; Reference number: I56100; MUID: 91201892
                                                                                                                                                          A; Title: Cloning of the 1.4-kb mRNA species of human complement factor H reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation; NMR structure determination, residues 264-292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 19-20, 'Q', 22-29, 'V', 31-33, 'Q', 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 'METGRNHL
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A; Residues: 'DFRN', 57
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A;Accession: A54726
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A; Residues: 1-56;1177-1231 <EST>
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A;Status: not compared with conceptual translation
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F;1109-1163/Domain: complement factor H repeat homology <FH19>
F;1167-1228/Domain: complement factor H repeat homology <FH19>
F;1167-1228/Domain: complement factor H repeat homology <FH20>
F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F;217-81043,839-864,870-915,901-926,931-973,959-984,989-1032,1018-1043,1048-1091,1077-F;217/Binding site: carbohydrate (Asn) (covalent) #status experimental F;529,802,822,882,911/Binding site: carbohydrate (Asn) (covalent) #status predicted F;718,1029,1095/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;753-803/Domain:
F;811-864/Domain:
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NBHUHS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;448-505/Domain:
F;509-564/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;325-385/Domain:
F;389-442/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;85-141/Domain: complement factor H repeat homology <FH02> F;146-205/Domain: complement factor H repeat homology <FH03:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;870-926/Domain: complement factor H repeat homology <FH15>;931-984/Domain: complement factor H repeat homology <FH16>;989-1043/Domain: complement factor H repeat homology <FH17>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;870-926/Domain:
;931-984/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;569-623/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: complement factor H; complement factor H repeat homology; Keywords: alternative splicing; complement alternate pathway; glycoprotein; 1.18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246-248/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267-320/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210-262/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-80/Domain: complement factor H repeat homology <FH01>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-1229/Product: complement factor H *status experimental <MPT>
19-449/Product: complement factor H, short splice form *status experimental <MAT>
                                                                                                             439 TPRCIRVK 446
                                                                                                                                                               421 PPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                          319
                                                                                                                                                                                                                                                                                                                                                                                               301
                                                                                                                                                                                                                                                                                                                                                                                                                                                       259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 SNEKPQCVEISCLPPRVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                          ω
                                                                                                                                                                                                                                                                         WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                                                                                                                                       WSPAVPCLRKCYFPYLENGYNQNHGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP
                                                                                                                                                                                                                                                                                                                                                                                      RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                 LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSR 60
                                                                                                                                                                                                                                                                                                                                    RCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWDHIHCTQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement factor H repeat homology <FH09>
complement factor H repeat homology <FH10>
complement factor H repeat homology <FH11>
complement factor H repeat homology <FH12>
complement factor H repeat homology <FH13>
complement factor H repeat homology <FH13>
complement factor H repeat homology <FH13>
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complement factor H repeat
complement factor H repeat
complement factor H repeat
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complement factor H repeat homology <FH04>
cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1714; DB 1
Pred. No. 4.5e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology <FH08>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nomology <FH06> homology <FH07>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    homology <FH05>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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complement

factor H precursor,

short splice

form -

A; Description: a cofactor in the inactivation of C3b

by serine proteinase I;

also

C; Function

```
A; Molecule type: mRNA
A; Residues: 'II', '55-401,'Y', 403-449 <SCH>
A; Residues: 'II', '55-401,'Y', 403-449 <SCH>
A; Note: an additional nuclectide present within the codon for Glu-310 was thought to
R; Schwaeble, W.; Zwirner, J.; Schulz, T.F.; Linke, R.P.; Dierich, M.P.; Weiss, E.H.
Eur. J. Immunol. 17, 1485-1489, 1987
Eur. J. Immunol. 17, 1485-1489, 1987
A; Title: Human complement factor H: expression of an additional truncated gene produc
A; Reference number: A61103; MUID: 88055295
A; Accession: A61103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-33;434-449 <EST>
A;Residues: 1-3;434-449 <EST>
A;Residues: 1-3;434-449 <EST>
A;Rote: only portions of this 1.8 kilobase mRNA were sequenced
R;Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P.
Eur. J. Immunol. 16, 1351-1355, 1986
Bur. J. Immunol. 16, 1351-1355, 1986
A;Title: Human complement factor H: isolation of cDNA clones and partial cDNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Kristensen, T.; Wetsel, R.A.; Tack, B.F.
J. Immunol. 136, 3407-3411, 1986
A;Title: Structural analysis of human complement protein
A;Reference number: S10479; MUID:86169701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 19-20, 'Q', 22-29, 'V', 31-33, 'Q', 35
R; Barlow, P.N.: Norman, D.G.; Steinkasserer,
Biochemistry 31, 3626-3634, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X07523; EMBL:Y00716; NID:g32492; A;Note: part of this sequence, including the amino end of A;Note: 402-Tyr was also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: complement factor H-related protein; complement protein H C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change 22-Jun-1999
C;Accession: S03013; B60238; A27877; A61103; A26505; S10479
R;Ripoche, J.; Day, A.J.; Harris, T.J.R.; Sim, R.B.
Biochem. J. 249, 593-602, 1988
       A; Note:
                                      A; Cross-references: GDB:129095
A; Map position: 1q32-1q32
                                                                                                                                                                                                                                                                                                         C; Genetics:
                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M12383; NID:g180472; PIDN:AAA52013.1; PID:g180473 C;Comment: Factor H has also been found bound to cell membranes in an un C;Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are exp
                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 226-401, Y, 403-449 < KRI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A44551; MUID: 92232649 A; Contents: annotation; NMR structure determination,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A26505; MUID:83048213 A;Accession: A26505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: this is a partial sequence of an alternatively spliced 1.8 kil R;Sim, R.B.; Discipio, R.G. Biochem. J. 205, 285-293, 1982
A;Title: Purification and structural studies on the complement-system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A27877; MUID:87054207 A; Accession: A27877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eur. J. Immunol. 21, 799-802, 1991
A; Title: Human complement factor H: two factor H proteins A; Reference number: A60238; MUID:91184292
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                                                                                                                   A; Gene: GDB: HF2; HF
                                                                                                                                                          C; Genetics:
                                                                                                                                                                                             A; Map position:
                                                                                                                                                                                                                            A; Cross-references: GDB:120041;
                                                                                                                                                                                                                                                                  A; Gene: GDB: HF1; HF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S10479
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 27-76 <SC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: B60238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S03013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-449 < RIP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
   the correspondence between
                                                                                                                                                                                                                                                                                                         <HF1>
                                                                                                                                                      <HF2>
                                                                                                                                                                                     1932-1932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steinkasserer, A.; Horne,
the two loci and the sequences indicated is unclea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <SIM>
                                                                                                                                                                                                                                                                                                                                    to cell membranes in an unknown mand 1.4 kilobases are expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the mature protein was conf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAA30403.1; PID:g75807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               homology with C4b binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           264-292
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                                                                                                                                                                                                                                                                                                                                    an unknown manner.
re expressed in liv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.; Driscoll, P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                example of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           control protein
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C;Species: Bos primigenius faurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S65551
R;Soames, C.J.; Day, A.J.; Sim, R.B.
Blochem. J. 315, 523-531, 1996
A;Title: Prediction from sequence comparisons of residues of factor H involved A;Reference number: S65551; MUID:96202005
A;Accession: S65551
A;Accession: S65551; MUID:96202005
A;Accession: S65551; MUID:96202005
A;Residues: preliminary; not compared with conceptual translation
A;Residues: 1-669 <SOA>
A;Residues: 1-669 <SOA>
A;Cross-references: GB:X98697; NID:g1419423; PIDN:CAA67257.1; PID:g1419424
C;Superfamily: complement factor H; complement factor H repeat homology <FHR1>
F;296-349/Domain: complement factor H repeat homology <FHR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     he alternative complement pathway
A;Pathway: complement alternate pathway
C;Superfamily: complement factor H; complement alternate pathway; glycoprotein; plasma
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-449/Product: complement factor H, short splice form #status experimental <MAT>
F;85-141/Domain: complement factor H repeat homology <FH01>
F;85-141/Domain: complement factor H repeat homology <FH03>
F;146-205/Domain: complement factor H repeat homology <FH04>
F;210-262/Domain: complement factor H repeat homology <FH04>
F;267-320/Domain: complement factor H repeat homology <FH05>
F;267-320/Domain: complement factor H repeat homology <FH05>
F;267-320/Domain: complement factor H repeat homology <FH06>
F;352-385/Domain: complement factor H repeat homology <FH06>
F;319-442/Domain: complement factor H repeat homology <FH07>
F;31-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F;217/Binding site: carbohydrate (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $65551
factor H - bovine (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          421 PPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               259 LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TPRCIRV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WSPAVPCLRKCYFPYLENGYNQNHGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SNEKPQCVEISCLPPRVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCTLXPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWDHIHCTQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
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67.48;
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Pred. No. 3.
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Db Db

75

296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLR 355

74

WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYRCDNGFSPPSGYSWDYLR

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A,Note: translation of the nucleotide sequence is not complete C;Superfamily: complement factor H; complement factor H repeat homology F;28-81/Domain: complement factor H repeat homology <FH1> F;86-146/Domain: complement factor H repeat homology <FH2> F;150-203/Domain: complement factor H repeat homology <FH3> F;209-266/Domain: complement factor H repeat homology <FH4> F;209-266/Domain: complement factor H repeat homology <FH4> F;209-266/Domain: complement factor H repeat homology <FH5> F;332-386/Domain: complement factor H repeat homology <FH6> F;390-451/Domain: complement factor H repeat homology <FH7>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement factor H-related protein 3A4/5G4 - mouse (fragment) (Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 27-Jul-1990 *sequence_revision 31-Dec-1993 *text_change 20-Aug-1999 (C;Accession: A3506B; B3506B; C3506B; B3506B; E3506B; E3506B; G3506B R;Vik, D.P.; Munoz-Canoves, P.; Kozono, H.; Martin, L.G.; Tack, B.F.; Chapl. J. Biol. Chem. 265, 3193-3201, 1990
Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A35070; MUID:90153969 A; Accession: A35068
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A;Title: Identification and sequence analysis of four complement factor H-related tra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M29010; NID:g192561; PIDN:AAA37415.1; PID:g387128
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-452 <VIK>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   183
  236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          123 VILNGQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLYY--SYRGYFPARVNQQFVYSCDHHFVPPSQRSWDHLACTAEGWSPEEPCLRQCIFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCIFHY 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGVYRPELSKYRGQDKITYECKKGFFPEIRGTDATCTRDGWVPVPRCAWKPCSYPVIKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAPRCSLKPCDFPQFKHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSPHLAEGNQFEYGAKYVYTCDEGYQMYGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDIPICEVVKCLPVTELE 135
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                                                                                   Similarity
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                                                       Conservative
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71.0%;
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                                                    18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kozono, H.; Martin, L.G.; Tack, B.F.; Chaplin, D.D.
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                                                                                Score 813; DB 2;
Pred. No. 1.2e-49;
                                                          38;
                                                                                                         Length 452;
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A; Residues: 1-303 <VIK>
A; Residues: 1-303 <VIK>
A; Cross-references: GB:M29007; NID:g192557; PIDN:AAA37413.1; PID:g309164; GB:J05259
A; Note: translation of the nucleotide sequence is not complete
C; Superfamily: complement factor H repeat homology
C; Keywords: duplication
F; 28-81/Domain: complement factor H repeat homology <FH01>
F; 86-146/Domain: complement factor H repeat homology <FH02>
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                                                                                                                                                                                                                                                   probable complement regulatory plasma protein SB1 - barred sand bass C;Species: Parablax neblifer (barred sand bass) C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 08-oc C;Accession: S46199; S77894
R;Dahmen, A.; Kaldoh, T.; Z19fel, P.F.; Gigli, I.
Blochem. J. 301, 391-397, 1994
A;Title: Cloning and characterization of a cDNA representing a putati
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A;Title: Identification and sequence analysis of four complement factor H-related transcape number: A35070; MUID:90153969
A;Accession: H35068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                              A; Molecule type: mRNA
A; Residues: 1-1053 < CAH1>
A; Cross - references: EMBL:L21703;
A; Experimental source: liver
                                                                                                                                                                                             A; Reference number: $46199; MUID:94318039
A; Accession: $46199
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A; Molecule type: protein
A; Residues: 526-532, 'X', 534-537; 809-817, 'X', 819-826 <DAH2>
                                                         A; Accession: S77894
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NGWSPPPKCIRIK 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAQGWEPEVPCVRKCVFHYVENGDSTYWEKIYVQGQSLKVQCYNGYSLQNGQDTMTCTE 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPSGYSWDYLR
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                                                                                                            NID: g639894;
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Pred. No. 1.1e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                  PIDN: AAA92556.1;
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                                                                                                                                                                                                                                                                                                                                                                            #text_change 08-Oct-1999
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                                                                                                                  PID:g639895
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A;Gene: SB1
C;Superfamily: complement factor H repeat homology
C;Keywords: glycoprotein
F;89-145/Domain: complement factor H repeat homology <FH01>
F;334-389/Domain: complement factor H repeat homology <FH02>
F;345-502/Domain: complement factor H repeat homology <FH03>
F;69-624/Domain: complement factor H repeat homology <FH03>
F;682-738/Domain: complement factor H repeat homology <FH04>
F;743-802/Domain: complement factor H repeat homology <FH05>
F;943-802/Domain: complement factor H repeat homology <FH05>
F;943-989/Domain: complement factor H repeat homology <FH05>
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561
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  ICTLRADVCGPPPE
                                                                                               TTCGKFPEIPNAEVI---RRYPEVQTVQVICNQGYS--TQANSFSCENGNWLLYGLSPDQ 560
                                                                                                                                           ----FHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGW------
                                                                                                                                                                                                 NGFF'---RGPY----TGRVLYYTCKDGYKLFTEGWWAEAKCVDGVW----PELTTCISN 505
                                                                                                                                                                                                                                             GRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCI--
                                                                                                                                                                                                                                                                                              NIQDAVIVGTDKQIYNLNQKAIYACGEGNRGRITLTCGENGWSGDRKCTVKPCPLPPKDP 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                 -PHRI-----KHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRYEPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRCSNR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGGPE----EATFGNVVRFSCKSRSEILLDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQC-PLIHVDNNVQV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDIPICEVVKCLPVTELENGRIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EASYPGGRQVRVGCNVGYS--GFFKLVCVEGKWETRGAK--CQPRSCGHPGDAQFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                RPEHVDSWDVRSWERYTLDDNTRYWCKRGYKRTGGVTWATCGRNGWMPNPLCEVKTCSKE
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                                                 -----SPPPK 423
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  574
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complement factor H-related protein 9C4 - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (C;Species: Mus musculus (house mouse) (C;Date: 27-Jul-1990 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999 (C;Accession: D35069; A35070; B35070; C35070; D35070; E35069; E35070; F35069; F35070; C;Accession: D35069; A35070; B35070; C35070; Martin, L.G.; Tack, B.F.; Chaplin, D.D. R.Vik, D.P.; Munoz-Canoves, P.; Kozono, H.; Martin, L.G.; Tack, B.F.; Chaplin, D.D. J. Biol. Chem. 265, 3193-3201, 1990
J. Biol. Chem. 265, 3193-3201, 1990
A;Title: Identification and sequence analysis of four complement factor H-related transference number: A35070; MUID:90153969

A; Molecule type: mRNA A; Residues: 1-808 <VII

<VIK>

Status: preliminary

A;Cross-references: GB:M29009; NID:g192563; PIDN:AAA37416.1; PID:g309166; GB:J05259

A; Reference number: A; Accession: D35069

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A; Cross references: EMBD: 235490
A; Cross references: EMBD: 235490
C; Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology <FF1>F; 50-107/Domain: complement factor H repeat homology <FF12>F; 112-169/Domain: complement factor H repeat homology <FF13>F; 174-234/Domain: complement factor H repeat homology <FF14>F; 239-294/Domain: complement factor H repeat homology <FF15>F; 239-294/Domain: complement factor H repeat homology <FF15>F; 364-422/Domain: complement factor H repeat homology <FF15>F; 364-422/Domain: complement factor H repeat homology <FF17>F; 484-538/Domain: complement factor H repeat homology <FF18>
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Biochim. Biophys. Acta 1261, 285-289, 1995
A;Title: cDNA structure of rabbit C4b-binding protein alpha-chain.
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C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
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F;332-346/Domain: complement factor H repeat homology <FH07>
F;455-305/Domain: complement factor H repeat homology <FH08>
F;511-564/Domain: complement factor H repeat homology <FH09>
F;569-622/Domain: complement factor H repeat homology <FH10>
F;680-742/Domain: complement factor H repeat homology <FH110>
F;680-742/Domain: complement factor H repeat homology <FH11>
F;746-807/Domain: complement factor H repeat homology <FH12>
F;746-807/Domain: complement factor H repeat homology <FH13>
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A; Accession: S53711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; nucleic acid sequence not shown
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Best Local
   116 WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              348 QSYMDYLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNG 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              288 VSKCTITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPS 347
                                                                                                                                  60
                                                                                                                                                                                               49
                                                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                            2 DCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLG-TIVKVCK-NGEWVPSNPS 59
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                                                            TFCVKKRCRNPGDLPNG--QVEVKTDFSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVE 161
                                                                                                                      RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDAD----G 115
                                                                                                                                                                                     DC-GPPPHLLFASSISELSENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW----SYD 104
                                                                                                                                                                                                                                                                                                                     148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QDTMTCTENGWSPPPKCIRIK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLFWDYLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LSNILLTAWLSTAKGEVKSCEFPQFKYGRLYFEEILRPNFPVSIGNKYSYKCDNGFSPPS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1-597 <DEF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                           21.6%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23.1%;
                                                                                                                                                                                                                                                                                                                  63;
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                                                                                                                                                                                                                                                                                                                                              Score 529.5; DI
Pred. No. 1e-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 566; DB 2
Pred. No. 4e-32;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                               187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27;
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                                                                                                                                                                                                                                                                                                                                                                        Length 597;
                                                                                                                                                                                                                                                                                                           Indels 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                           26;
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A; Molecule type: DNA
A; Residues: 203-288 <LIN>
A; Cross-references: EMBL: X04284; EMBL: X04296
R; Rodriguez de Cordoba, S.; Sanchez-Corral, P.;
J. Exp. Med. 173, 1073-1082, 1991
                                                                                                                                                                                                                      A; Title: Studies on the structure of the human A; Reference number: A24182; MUID:86301119
                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 80-597 <CH2>
A; Cross references: GB:X02865; NID:g29564;
A; Note: 92-Thr and 357-H1s were also found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A:Note: although the sequence determined extends to residue 9 above, these authors as R;Chung, L.P.; Bentley, D.R.; Reid, K.B.M.
Biochem. J. 230, 133-141, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M31452; NID:g190501; PIDN:AAA36507.1; PID:g190502 A;Note: the authors translated the codon GGA for residue 492 as Glu R;Lintin, S.J.; Lewin, A.R.; Reid, K.B.M. FEBS Lett. 232, 328-332, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A33568; S02372; A90326; A24182; A93134; S29492; A31785; I52244; A03210
R;Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y.
Blochem. Blophys. Res. Commun. 165, 138-144, 1989
A;Title: Molecular cloning of the cDNa coding for proline-rich protein (PRP): identit A;Reference number: A33568; MUID:90073699
A; Title:
                                                                                                                                                                                     A; Accession: A24182
                                                                                                                                                                                                                                                                                      R; Lintin, S.J.; Reid, K.B.M. FEBS Lett. 204, 77-81, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A90326; MUID:86025405 A; Accession: A90326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Derivation of the sequence of the signal peptide in human C4b-binding protei A;Reference number: S02372; MUID:88242821
A;Accession: S02372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: X07853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 17-81 <LI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-597 <MA1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N; Alternate names: C4BP; proline-rich protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4b-binding protein alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     рЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  505 ENLTVRCDSGYGVV-GSPSITCTENRNWQPEVPKC 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 QSAKVQCHSGYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279 IHCELDSKWNPSPPVCESNSCLGLPNVPHASQQGYQWSTKEGVYS------VGTELRYK 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      162 WSDPLPKCEIVKCEPPPNIINGKHNGG---NEDIHTYGSSVTYSCNPRFSLLGEASISCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   388 TYFFGDIVVYSCYQKQRTTVTCRADGTWSPHTPLCGPSCDSPPPIAHGYHTPVSSVLSFT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               332 CRPGYRPVADEPI---IVTCQEDLRWSPFAGCEAICCPHPQLDNGAI-TEHSRNPRANNC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              231 AVC-TGSGWNPQPS-CEEMTCL-TPYIPN------GIYTPHRIKHRIDDEIRYE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176 EN----GLWSNEKPQCVEISCLPPRVENGDGIY-LKPVYKENERFQYKCKQGFVYKERGD 230
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                                                  Rey-Campos,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the cDNA coding for C4b-binding
                                                                                                                                                                                                                                                    protein gene
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Structure of the gene coding for the alpha polypeptide chain of the human co

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C;Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein; F;1-48/Domain: signal sequence #status predicted <SIG> F;49-597/Product: C4b-binding protein alpha chain #status predicted <MAT> F;50-108/Domain: complement factor H repeat homology <FH1> F;113-170/Domain: complement factor H repeat homology <FH3> F;175-234/Domain: complement factor H repeat homology <FH4> F;239-294/Domain: complement factor H repeat homology <FH4> F;299-360/Domain: complement factor H repeat homology <FH5> F;299-360/Domain: complement factor H repeat homology <FH5> F;399-364-422/Domain: complement factor H repeat homology <FH5> F;381-404/Region: complement factor H repeat homology <FH7> F;381-404/Region: complement factor H repeat homology <FH7> F;381-404/Region: complement factor H repeat homology <FH7> F;484-538/Domain: complement 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB.M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500
C;Comment: C4BP controls the classical pathway of complement activation. It binds as a checked the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement from C;Comment: C4BP occurs in plasma in two forms, both of which bind complement fragment C4 isulfide bonds. The beta chain binds the vitamin K-dependent plasma protein S. A minor fine control of the capacity of the capacity
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A;Residues: 381-404 CHES>
R;Suzuki, K.; Nishioka, J.
J. Biol. Chem. 263, 17034-17039, 1988
A;Title: Binding site for vitamin K-dependent protein S on complement C4b-binding protein R;Reference number: A31785; MUID:89034204
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A;Title: The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein is A;Reference number: S29492; MUID:93146164
A;Accession: S29492
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A; Contents: annotation; exon-intron boundaries
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A;Title: Genomic organization of the alpha chain of the human C4b-binding protein gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Complex: octamer of seven alpha chains and one beta chain C; Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 1q32-1q32
A; Introns: 48/1; 110/1; 1
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A; Residues: 1-597 <ASO>
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A; Accession: I52244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 495-505, 'X', 507-510, 'X', 512-515 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:120568; OMIM:120830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                actors V and VIII
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                                                                         Query Match
Best Local
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                                                                 Local Similarity
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22, 427-435, 1985
                                                                                                                                                                                                                                                                                                                                               site: carbohydrate (Asn) (covalent) #status experimental
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19.6%; Score 481.5; DB 1; 26.5%; Pred. No. 2.3e-26; tive 78; Mismatches 195;
                                                                                                                                          Length 597;
       Indels
       99;
       Gaps
       25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;239-294/Domain: complement factor H repeat F;299-362/Domain: complement factor H repeat
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Matches Query Match Best Local

140;

Conservative

76;

Pred. No. 7.2e-Score 474.5; Mismatches

DB 1; 180;

Length

119;

Gaps

29;

homology

homology homology

<FH6> <FH5>

5 GPPPRENSEILSGSWSEQLYSEGTQATYKCRPGYRTLGTIVKVCKN-----GEWVPSN 57

GIPPYLDFAFPINELNETRFETGTTLRYTCRPGYR----ISSRKNFLICDGTDNW---K 102 PSRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEID-YRECDADG- 115

:: = ::

Local

Similarity

19.3**%**; 27.2**%**;

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C;ACCESSION, A.; Thern, A.; Dahlback, p. R;Hillarp, A.; Thern, A.; 190,4199, 1994

J. Immunol. 153, 4190-4199, 1994

A;Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains

A;Title: Bovine C4b binding protein. Molecular cloning of the alpha- and beta-chains
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                                                                                                                                                                                                                                                                                                                                            C4b-binding protein alpha chain - bovine C;Species: Bos primigenius taurus (cattle) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: I46001; S43190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Qy
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                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-610 <HIL>
                                            F;112-169/Domain: complement factor
                                                                   C;Superfamily: C4b-binding protein alpha chain; complement factor F;50-107/Domain: complement factor H repeat homology <FHl>
                                                                                                                     A; Cross-references: EMBL: Z31693; NID: g469117; PIDN: CAA83498.1; PID: g469118
                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYGVV-GPQSITCSGNRTWYPEVPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPATRSPVSKCTITG--WIPAPRCSLKPCDFPQFKHGRLYYEESRRP--------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VENETIGVWRPSPPTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVL--RGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WSHPLPQCEIVKCKPPPDIRNGR----HSGEENFYAYGFSVTYSCDPRFSLLGHASISCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -FCIYKRCRHPGELRNG--QVEIKTDLSFGSQIEFSCSEGFFLIGSTTSR-CEVQDRGVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCGPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWVYNT-- 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GYILVGQA----KLSCSYSHWSAPAPQCKALCRKPELVNGRLSVDKDQYVEPENVTIQCDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSCHETSRFSAICQGDGTWSPRTPSCGDICNFPPKIAHGHYKQSSSYSFFKEEIIYECDK 456
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KPTTDEPTTVICQKNLRWTPYQGCEALCCPEPKLNNGEITQHRKSRPANHCVYFYGDEIS 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SVIHCDADSKWNPSPPACEPNSCINLPDIPHASWETYPRPTKEDVYVVGTVLRYRCHPGY
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                                            H repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     538
homology <FH4>
                                                    homology <FH2>
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                                                                                                     H repeat homology
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F;1-18/Domain: Signal sequence #status predicted <SIG>
F;19-331/Product: complement factor H-related protein DOWN16 #status predicted <MAT>
F;29-83/Domain: complement factor H repeat homology <FH01>
F;87-141/Domain: complement factor H repeat homology <FH02>
F;147-204/Domain: complement factor H repeat homology <FH03>
F;211-265/Domain: complement factor H repeat homology <FH04>
F;311-265/Domain: complement factor H repeat homology <FH06>
F;369-330/Domain: complement factor H repeat homology <FH05>
F;169-330/Domain: complement factor H repeat homology <FH06>
F;108,186,206,310/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Superfamily: complement C3d/Epstein-Barr virus receptor; complement factor H repeat C;Keywords: glycoprotein
C;Keywords: glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-331 <SKE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: A novel short consensus repeat-containing molecule is related to human compleme A;Reference number: A45222; MUID:93155112
A;Accession: A45222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement factor H-related protein DOWN16 precursor - human C;Species: Homo sapiens (man) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Mar-2000 C;Accession: A45222; S29609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:X68679; NID:g30869; PID:g30870
A;Experimental source: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Skerka, C.; Kuhn, S.; Gunther, K.;
J. Biol. Chem. 268, 2904-2908, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: sequence extracted from NCBI backbone (NCBIP:124269)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δÃ
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                                                        353 YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-GQDTY 411
                                                                                                                                                                               293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
69 YIHCTQNGWSPAVPCLRKCYFPYLENGYNQNYGRKFVQGNSTEVACHPGYGLPKVRQTTV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 CS-EN---GLWSNEKPQCVEISCLPPRVENG---DGIYLKPYYKENERFQYKCKQGFVYK 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       508 EIITIQCESGYSVV-GSENITCSEDRTWYPEVPKC 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     448 TFDHQAVYECDKGYILVGAKELSCTSSGWSPAVPQCKALCLKPEIEYGRLSVEKVRYVEP 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         388 THCTYISGDKISYECHSKYMFDALCTKHGTWSPRTPECRPDCKSPPVIAHGQHKVVSKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  103 YKEFCVKKRCENPGELLNG--QVIVKTDYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGV 160
                                                                                                                                                                                                                                                                                    Local
                                                                                                                          9 LTLWVSCANGQVKPCDFPDIKHGGLFHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QSAKVQCHSGYSLPNGQDTYYCTEN-GWSPP-PKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTPSQSYWD-----YLRCTVNGWEPEVP-CLRQCIFHYVEYGESSYWQRRYIEG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SYKCHFGYKPETDGPT---TVTCQSNLEWSPYIECKEVCCPEPNLNNYGSITLHRRPSTS 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEGDSLIHCEADNSWNPPPPTCELNGCLGLPHIPHALW--ERYDHQTQTEQQVYDIGFVL 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERGDAV--C-TGSGWN-PQPSCEEMTCL-TPYIPNGIYTPHRIKHRIDDE-----I 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RYECKNGFYPATRSPVSKCTIT-----GWIPAPRCSLKPCDFPQF-KHG--RLYYEESRR 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRVENKTIGVWSPSPPSCKKVICVQPVVKDGKITSG--FGPIYTYQQSIVYACNKGF--R 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VWSDPLPQCIIAKCEPPPTISNGRHNGG----DEDFYTYGSSVTYSCDRDFSMLGKASIS 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -WINDIPICEVVKCLPVTELENGRIVSGAAEPDQEYY-FGQVVRFECNSGFKIEGQKEMH 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PYFPVPIGKEYSYYCDNG-----
                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                       19.0%; score 466.5; DB 2; Length 331; 56.3%; Pred. No. 1.3e-25;
                                                                                                                                                                                                                                                 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.; Lingelbach, K.; Zipfel, P.F.
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F:145-211/Domain: complement factor H repeat homology <FH03>
F:217-272/Domain: complement factor H repeat homology <FH03>
F:276-331/Domain: complement factor H repeat homology <FH05>
F:336-394/Domain: complement factor H repeat homology <FH05>
F:399-458/Domain: complement factor H repeat homology <FH05>
F:399-458/Domain: complement factor H repeat homology <FH07>
F:467-523/Domain: complement factor H repeat homology <FH08>
F:531-587/Domain: complement factor H repeat homology <FH09>
F:592-648/Domain: complement factor H repeat homology <FH109>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A:Introns: 80/1; 113/2; 142/1; 275/1; 333/1 c;Superfamily: complement factor H repeat homology F;22-78/Domain: complement factor H repeat homology <FH01>F;83-140/Domain: complement factor H repeat homology <FH02>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U17128; NID:g595980; PIDN:AAA78271.1; PID:g595988 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Experimental source: clone 31-1
R;Kim, Y.U.; Kinoshita, T.; Molina, H.; Hourcade, D.; Seya, T.; Wagner, L.M.; Holers, J. Exp. Med. 181, 151-159, 1995
A;Title: Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of A;Reference number: 148306; MUID:95105691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: Cr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The murine complement receptor gene family. IV. Alternative splicing of Cr2 A;Reference number: A45900; MUID:90229754
A;Accession: A45900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement C3b receptor type 2 long form precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 21-367 < RES>
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A; Residues: 1-676 < KUR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: A45900; I48306
R; Kurtz, C.B.; O'Toole, E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                     302 CSLKPCD-FP-QFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFT---TPSQSYWDYLRC 356
                                                                                                                    273 -FMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNTVPT 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 SGAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQCV-E 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 --IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDFY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    412 YCTENGWSPPPKCVR 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 SEFEFGAKVVYTCDEGYQLLGEIDYRECDADG---WTNDIPICEVVKCLPVTELENGRIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              129 TCTENGWSPTPRCIR 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42 FAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSVHINTG 99
                                                                                                                                                                                                                                                                                  VKCPMPEIENGLVESG--FKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPPLPTC
                                                                                                                                                                                                                                                                                                                                                             ISCLPPRVENG---DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC 244
                                                                                                                                                                                                   EEMTCLTPY-IPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WI-PAPR 301
                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSRD---SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPPPQCIPR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.5%;
ilarity 28.6%;
Conservative 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 453; DB 2; Length 676; Pred. No. 2.6e-24;
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F;17-134/Domain: complement factor H repeat homology <FH2>
F;139-199/Domain: complement factor H repeat homology <FH3>
F;139-199/Domain: complement factor H repeat homology <FH4>
F;204-258/Domain: complement factor H repeat homology <FH4>
F;263-324/Domain: complement factor H repeat homology <FH6>
F;328-386/Domain: complement factor H repeat homology <FH6>
F;390-443/Domain: complement factor H repeat homology <FH7>
F;447-501/Domain: complement factor H repeat homology <FH8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4BP protein alpha chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change
C:Accession: S57953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Z50051; NID:g899379; PIDN:CAA90391.1; PII C;Superfamily: C4b-binding protein alpha chain; complement factor F;15-72/Domain: complement factor H repeat homology <FHI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
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Best Local :
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420 GYRLVGEATISCWYSQWTPAAPQCKALCRKPEIGNGVLSTNKDQYVETENVTIQCDSGFV
                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        438 AIFCISENQVHATWDKAPPIC 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      410 TYYC-TEN----GW-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 331
                                                                                                                                                                                    308 M---TVICQKDLSWSMLRGCKEICCPVPDPKSVRVIQHEKAHPDNDCTYF---FGDEVSY
                                                                                                                                                                                                                               288 VSKCTI----TGWIPAPRCSLKPCDFPQFKHGRLYYEESRRP----YFPVPIGKEYSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73 VKKSCRNPGDLQNG--KVEVKTDFLFGSQIEFSCSEGYILIGSSTSYCEIQGKGVSWSDP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 GPPPRENSEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVCKN-GEWVPSNPSRIC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLG-EIDYRECDADG--WTND 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPPPDLPYALPASEMNQTDFESHTTLRYNCRPGYSRASSSQSLYCKPLGKW----QINIAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CEVKSCDAIPNHLLHGRVFLPPN-----LQLGAEVSFVCDLGFQLKGKPSS-----
                                                                                                                                                                                                                                                                          {\tt ADGSWSPVPVCELNSCTDIPDIPNAALITSPRPRKEDVYPVGTVLRYICRPGYEPATRQP}
                                                                                                                                                                                                                                                                                                                      GSG-WNPQPSCEEMTCL-TPYIPNG--IYTPHRIK---HRIDDEIRYECKNGFYPATRSP
                                                                                                                                                                                                                                                                                                                                                                      TVGVWSPSPPTCERIICPWPKVLHGTINSGFKHTYKYKDSVRFVCQKGFVLRGSGVIHCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPECVIAKCGMPPDISNGK---HNGREEEFFTYRSSVTYKCDPDFTLLGNASITCTVVNK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPEGETVIWNNKFPVCEQISCDPPPEVKNARKPYYSLPIVPGTVLRYTCSPSYRL-IGEK 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVNG----WEPEVPCLRQCIFH---YVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQD 409
                                                                                                                                                                                                                                                                                                                                                                                                                 ENGLWSNEKPQCVEISCLPPRVENGD-GIYLKPVYKENERFQYKCKQGFVYKERGDAVCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-558 <HIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                             -CTVNGWEPEVP-CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYS 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 4e-
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN:CAA90391.1; PID:g899380
                                                                                                                                      -GFTTPSQSYWDYLR------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175
                                                                                                                                                                                                                                                                                                                                                                      247
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                QY
                                                                   DЬ
                                                                                                            δÃ
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F:18-74/Domain: complement factor H repeat homology <FH01>
F:79-136/Domain: complement factor H repeat homology <FH02>
F:79-136/Domain: complement factor H repeat homology <FH03>
F:141-207/Domain: complement factor H repeat homology <FH03>
F:213-268/Domain: complement factor H repeat homology <FH05>
F:272-328/Domain: complement factor H repeat homology <FH05>
F:373-391/Domain: complement factor H repeat homology <FH06>
F:333-391/Domain: complement factor H repeat homology <FH06>
F:333-391/Domain: complement factor H repeat homology <FH08>
F:470-526/Domain: complement factor H repeat homology <FH09>
F:429-586/Domain: complement factor H repeat homology <FH10>
F:722-778/Domain: complement factor H repeat homology <FH10>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: CR1
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C;Keywords: duplication; glycoprotein; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;1041-1107/Domain: complement factor H repeat homology <FH11>
F;1172-1228/Domain: complement factor H repeat homology <FH12>
F;1173-1228/Domain: complement factor H repeat homology <FH12>
F;1233-1291/Domain: complement factor H repeat homology <FH13>
F;1296-1362/Domain: complement factor H repeat homology <FH15>
F;1432-1489/Domain: complement factor H repeat homology <FH15>
F;1625-1681/Domain: complement factor H repeat homology <FH16>
F;1749-1815/Domain: complement factor H repeat homology <FH17>
F;1749-1815/Domain: complement factor H repeat homology <FH17>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-397,1751-2014 <BIR2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Accession: I36937
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: I36935; MUID:94292799
A; Accession: I36936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P. J. Immunol. 153, 691–700, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Species: Pan troglodytes (chimpanzee) C; Date: 02-Jul-1996 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement receptor 1 - chimpanzee (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1823-1879/Domain: complement F;1884-1940/Domain: complement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L24920; NID:g551564; PID:g557725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-2014 <BIR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Primary sequence of an alternatively spliced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: 136936; 136937
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1169 SRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSCEPG-YDLRGAASLHCTPQGDWSPEAPR
                                                                                                                                                                                                                                                                                              1055
                                                                        245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     941 GTSLKYECRPEYYGRPFSITCLDNLVW--SSPKDVCRRKSCKTPPDPVNG--MVHVITDI 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        404 LPNGQDTYYCTENG-WSP------PPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF
                                                                EEMTCLTPYIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIP-APR 301
                                                                                                                                                                                                                                                                                          TNRE---NFHYGSVVTYRCNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN 111:
                                                                                                                                                                                                                                                                                                                                                               GAAEPDQEYYFGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                                                                                                                                                                                        QVGSRINYSCTTGHRLIGH-SSAECILSGNSAHWSTKPPICQRIPCGLPPT-IANGDFIS 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M-LGSQSITCSENGTWYPKVSRCEQEVPKDCEHV
                                                                                                                                             KCTPPNVENGILVSDN---RSLFSLNEVVEFRCQPGFVMKGPHRVKCQALNKWEPELPSC
                                                                                                                                                                                                              SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 30.:
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18.2%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2014;
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                                                                                                                                             1168
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Search completed: November 21, 2000, 16:47:45 Job time: 374 sec

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Result
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Maximum
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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         900
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Ripoche J., Day A
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                                                                                                        SEQUENCE OF 53-445 FROM N.A. MEDLINE; 87054207.
Schulz T.F., Schwaeble W., S
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                                                                                                                                                              che J., Day A.J., Harris T.J.R., complete amino acid sequence of hem. J. 249:593-602(1988).
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                                                     J. Immunol. 16:1351-1355(1986).
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s (Human).

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MEDLINE; 83040211.

Sim R.B., Discipio R.G.;

"Purification and structural stude protein beta 1H (Factor H).";

Biochem. J. 205:285-293(1982).
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J. Mol. Biol. 232:268-284(1993).
-I. FUNCTION: FACTOR H FUNCTIONS AS A COFACTOR IN THE INACTIVATION C3B BY FACTOR I AND ALSO INCREASES THE RATE OF DISSOCIATION OF C3BBB COMPLEX (C3 CONVERTASE) AND THE (C3B) NBB COMPLEX (C5 CONVERTASE) IN THE ALIENNATIVE COMPLEMENT PATHWAY.
-I. SIMILARITY: CONTAINS 20 SUSHI (SCR) REPEATS.
-I. CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 341 ONWARD DUE TO A FRAMESHIFT.
   PFAM; PF00084; sushi; ZU.

Complement alternate pathway; Plasma; Glycoprotein; Signal; 3D-structure; Polymorphism.

1 18
COMPLEMENT FACTOR H.
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entities
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"Solution structure of the fifth repeat of factor of the complement control protein module.";
Biochemistry 31:3626-3634(1992).
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Barlow P.N., Steinkasserer A., Norman D.G., Kieffer
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D.G., Barlow
                                                                                                                                                                                                                                                                     non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                               RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG
                                                                                                                                                                                                                                                                                                                                                                                                                SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PICEVVKCLPYTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                             Eutheria;
                                                                                                                   (Rel. 02, Created)
(Rel. 27, Last sequence update)
(Rel. 35, Last annotation update)
PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA;
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                                                               Primates;
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67.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47;
        Aso T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1714;
Pred. No. 6
                                                                                                                                                                            PRT;
                                                              Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C65EC8CF8800B3FD CRC64;
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        Sata
                                                                                                                                                                            597 AA
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     Τ.,
                                                                         Vertebrata; Euteleostomi;
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                                                              Hominidae;
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        Niho Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1231;
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Chung L.P., Bentley .....
Chung L.P., Bentley .....
"Molecular cloning and characterization."
"Molecular cloning and characterization."
binding protein, a regulatory protein of the human complement system.";
ninchem. J. 230:133-141(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 85295001.

Chung L.P., Gagnon J., Reid K.B.M.;

Pamino acid sequence studies of human C4b-binding protein: N-terminal sequence analysis and alignment of the fragments produced by limited sequence analysis and alignment of the peptides produced by cyanogen
                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PICC. NAIL ACAG. SCI. U.S.A. 80:3461-3465(1993).

-i- FUNCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERPASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN S AND WITH SERUM AMYLOID P COMPONENT.

-i- SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP ALPHA AND BETA CHAINS OF 3 POSSIBLE SORTS: A 570 KDA COMPLEX OF 7 ALPHA CHAINS AND 1 BETA CHAIN, A 530 KDA HOMOHEDTAMER OF ALPHA CHAINS OR A 500 KDA BETA CHAIN, A 530 KDA HOMOHEDTAMER OF ALPHA CHAINS OR A 500 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Visualization of human C4b-binding protein and its complexes with vitamin K-dependent protein S and complement protein C4b."; Proc. Natl. Acad. Sci. U.S.A. 80:3461-3465(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular cloning of the cDNA coding for proline-rich protein (PRP): identity of PRP as C4b-binding protein.";
Biochem. Biophys. Res. Commun. 165:138-144(1989).
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
-!- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-17 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELECTRON MICROSCOPY, 3-DIMENSIONAL STRUCTURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4b-binding
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"Derivation of the sequence of the signal peptide in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 9-81 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun. 174:222-227(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Immunol. 22:427-435(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aso T., Okamura S., Matsuguchi T., "Genomic organization of the alpha
                                                                                                                                                                                                                                                                                                                                                           TISSUE SPECIFICITY: CHYLOMICRONS IN THE PLASMA
                                                                                                                                                                                                                                                                                                                                                                                              THE ALPHA CHAIN HOMOPOLYMER SUPPORTS TENTACLES, EACH WITH THE BINDING SITE FOR C4B AT THE END.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEX OF 6 ALPHA CHAINS AND 1 BETA CHAIN. THE CENTRAL
                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith C.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        characterization of the cDNA coding for C4b-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mueller-Eberhard H.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human C4b-binding
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                        moved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            classical pathway of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND LIGAND BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                              restrictions on
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MIM; 120830;
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                                                                                                   Local Similarity
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M624786; AAA36506.1;
M624776; AAA36506.1;
M624777; AAA36506.1;
M624777; AAA36506.1;
M624778; AAA36506.1;
M62478; AAA36506.1;
M62481; AAA36506.1;
M62481; AAA36506.1;
M62481; AAA36506.1;
M62482; AAA36506.1;
M62484; AAA36506.1;
M62485; AAA36506.1;
M62484; AAA36506.1;
M62485; AAA36506.1;
M62485; AAA36506.1;
M62485; AAA36506.1;
M62486; CAB51244.1;
X04296; CAA27839.1;
X04296; CAA27839.1;
 RICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDAD----G
                            NCGPPPTLSFAAPMDITLTETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWVYNT--
                                                      DCKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGY-RTLGTIVKVC-KNGEWVPSNPS
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                                                                                      Conservative
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                                                                                                  19.6%;
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                                                                                                                                                                                                                                                                                                  C4B-BINDING PROTEIN ALPHA CHAIN.

8 x SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 5.

SUSHI 6.

SUSHI 6.

SUSHI 7.

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SYMILARITY.

BY SIMILARITY.

BY SIMILARITY
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INTERCHAIN (WITH E
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                    Score 481.5; DB 1
Pred. No. 1.7e-29;
8; Mismatches 195
                                                                                                                                                                                                                   N-LINKED
Q -> T.
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                                                                                                                                                                                                    /FTId=VAR_001977
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                                                                                                                                                             67E03F2EA85A16DD
                                                                                                                                                                                                                               DB 1;
                                                                                      195;
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BETA CHAIN)
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                                                                                                                 Length
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal;
                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                    99;
                                                                                   Gaps
                            106
                                                         59
                                                                                      25;
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or send

an email

to license@isb-sib.ch).

(See http://www.isb-sib.ch/announce/

and

for

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entities requires a license agreement

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C4BP
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Q28065;
                                                                                                                                                                                                                                                                                                                                        formation with protein S.",

J. Immunol. 153:4190-4199(1994).

J. Immunol. 153:4190-4199(1994).

FUNCTION: C4BP CONVERDLY THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CONVERTASE) BY DISSOCIATING THE COMPLEMENT BERUM ANYLOID P COMPONENT.

FUNCTION OF C4BP ALPHA AND BETA CHAINS (BY SIMILARITY).
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Mammalia;
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
C4B-BINDING PROTEIN ALPHA CHAIN PRECUP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOVIN
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Embedding and the Embeddi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hillarp A., Thern A., Dahlbaech B.;
"Bovine C4b binding protein. Molecular cloning
beta-chains provides structural background for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
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                                                                                                                                                                                                                                                             SIMILARITY: TO C4BP BETA CHAIN AND TO PIG A SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
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                                                                                                SYKCHFGYKPETDGPT---TVTCQSNLEWSPYIECKEVCCPEPNLNNYGSITLHRRPSTS
                                                                                                                                        RYECKNGFYPATRSPVSKCTIT-----GWIPAPRCSLKPCDFPQF-KHG--RLYYEESRR
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                                                                                                                                                                                                                                                                                                              CS-EN---GLWSNEKPQCVEISCLPPRVENG---DGIYLKPVYKENERFQYKCKQGFVYK 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 474.5;
Pred. No. 5.9
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INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
INTERCHAIN (WITH BETA CHAIN) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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8 X SUSHI (SCR) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D806B270E8A06B58 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sushi; Signal
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                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
-!- SIMILARITY: CONTAINS 5 SUSHI (SCR) REPEATS
-!- SIMILARITY: STRONG, TO FACTOR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A novel short consensus repeat-containing molecule is related human complement factor H.";
J. Biol. Chem. 268:2904-2908(1993).
-i- FUNCTION: MIGHT BE INVOLVED IN COMPLEMENT REGULATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CFHD_HUMAN STANDARD; PRT; 331 AA. Q02985; 01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 01-JUN-1994 (Rel. 29, Last annotation update) COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR. Homo sapiens (Human).
                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                  PFAM; PF00084; sushi; 5. Repeat; Glycoprotein; Sushi;
                                                                                                                                                                                                                                                                                                                                                                                         PIR; A45222; A45222.
HSSP; P10998; 1VVC.
                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X68679; CAA48639.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skerka C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=LIVER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE; 93155112
353 YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-GQDTY 411
                                                                                                                                                                                                                                                                                                                                                                               INTERPRO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        508 EIITIQCESGYSVV-GSENITCSEDRTWYPEVPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  392 QSAKVQCHSGYSLPNGQDTYYCTEN-GWSPP-PKC
                                            9
                                         ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
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                                                                                                Similarity 56.3
76; Conservative
                                                                                                                                                                                                                                                                                                                                                                               IPR000436;
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                                                                                                                                                                    331 AA;
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331
331
85
128
207
265
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186
206
310
37469
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                                                                                                            19.0%;
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                                                                                                                                                                    WW;
                                                                                                                                                                         POTENTIAL.

COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16.

5 X SUSHI (SCR) REPEATS.

SUSHI 1.

SUSHI 2.

SUSHI 3.

SUSHI 4.

SUSHI 4.

SUSHI 5.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                18;
                                                                                                            Score 466.5; DB 1
Pred. No. 1.2e-28;
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                                                                                                                                                                  N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
3DC48293FD91332C CRC64
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                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lingelbach K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541
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01-NOV-1997
01-NOV-1997
15-JUL-1998
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between
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REPEAT
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hillarp A., Wiklund H., Thern A., Dahlback B., "Molecular cloning of rat C4b binding protein structural and functional relationships among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            structural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-SPRAGUE-DAWLEY; TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C4BPA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUSE, and rat proteins.";

Immunol. 158:1315-1323(1997).

TIMUCTION: C4BP CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINDS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. I ALSO ACCELERATES THE DEGRADATION OF THE C48C2A COMPLEX (C3 ALSO ACCELERATES THE DEGRADATION OF THE C48C2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINDS C4B. IT INTERACTS ALSO WITH ANTICOAGULANT PROTEIN AND WITH SERRIM ANYLOID P COMPONENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: DISULFIDE-LINKED COMPLEX OF C4BP A SIMILARITY: TO C4BP BETA CHAIN AND TO PIG A SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P10998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Z50051; CAA90391.1;
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Eutheria; Rodentia;
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(Rel. 35, Last sequence update)
(Rel. 36, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                sushi;
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      MIS AR
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Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
  Y SIMILARITY.
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among human,
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bovine, rabbit,
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Matches 137;
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P17927;
01-NOV-1990
01-NOV-1990
01-NOV-1997
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                                       Eutheria;
                                                        Metazoa;
                                                                                                                                  (Rel. 16, Created)
(Rel. 16, Last sequence update)
(Rel. 35, Last annotation update)
RECEPTOR TYPE 1 PRECURSOR (C3B/C4B
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[3]
                                                                      MOD_RES
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                                                                                                                                                                                                                                                                                                                                     between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no may modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Human C3b/C4b receptor (CR1). Demonstration of l repeating domains that are composed of the short characteristics of C3/C4 binding proteins."; J. Exp. Med. 165:1095-1112(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of distinct C3b and C4b recognition sites in the human C3b/C4b receptor (CR1, CD35) by deletion mutagenesis."; J. Exp. Med. 168:1699-1717(1988).
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BL; M11617; AAA52298.1; -.
BL; M11618; AAA52299.1; -.
BL; Y00816; CAA68755.1; -.
BL; X05309; CAA28333.1; -.
BL; X05309; CAA28333.1; -.
BL; X054748; A24748.
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R; B24748; C24748.
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POLYMORPHISM: CRI IS RESPONSIBLE FOR THE KNOPS BLOOD GROUP SYSTEM.
MISCELLANEOUS: SEVEN SHORT CONSENSUS REPEATS (SCR) CONSTITUTE A
LONG HOMOLOGOUS REPEAT (LHR). THE N-TERMINAL TWO SRCS OF LHR-A
CONTAINED A SITE DETERMINING C4 SPECIFICITY, AND THE N-TERMINAL
TWO SCRS OF LHR-B AND -C EACH HAD A SITE DETERMINING C3
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                                                                                                                                                  PRO; IPR000436; -.
PF00084; sushi; 30.
ement pathway; Glycoprotein; Transmembrane; Repeat; Signal;
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                                                         (SCR) REPEATS, LONG
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nes 132; Conserv
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                                                                                                                                                                                       SCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
                                                                                                                                                                                                                 TNRE----NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN
                                                                                                                                                                                                                                          GAAEPDQEYYFGQVVRFECNSG------FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                                                                                                                                   QFGSQIKYSCTKGYRLIGS-SSATCIISGDTVIWDNETPICDRIPCGLPPT-ITNGDFIS
                                                                                                                                                                                                                                                                                                                       GTYLNYECRPGYSGRPFSIICLKNSVWTGAKDR--CRRKSCRNPPDPVNGMVHVIKG--I 121
                                                                                                                                                                                                                                                                                                                                                GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF
    ---CVLAGMESLWNSSVPVCEQ--
                           YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN--
                                                                                                          SRV-CQPP--PDVLHAERTQRDKDNFSPGQEVFYSCEPG-YDLRGAASMRCTPQGDWSPA
                                                                                                                                 EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
                                                       APTCEVKSCDDFMGQLLNGRV-
                                                                                 APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD
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Pred. No. 1.6e-25
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C4BP_MC
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C4BP_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the serum complement system.";
BIOChemistry 26:4668-4674(1987).
-!- FUNCTION: C48P CONTROLS THE CLASSICAL PATHWAY OF COMPLEMENT ACTIVATION. IT BINUS AS A COFACTOR TO C3B/C4B INACTIVATOR (C3BINA), WHICH THEN HYDROLYZES THE COMPLEMENT FRAGMENT C4B. IT ALSO ACCELERATES THE DEGRADATION OF THE C4BC2A COMPLEX (C3 CONVERTASE) BY DISSOCIATING THE COMPLEMENT FRAGMENT C2A. ALPHA CHAIN BINUS C4B. IT INTERACTS ALSO WITH SERUM AMYLOID P COMPONENT.
-!- SUBUNIT: HOMOHEPTAMER; NOT COVALENTLY LINKED. MOUSE LACKS THE BETA CHAIN OF C4BP.
-!- SIMILARITY: TO C4BP BETA CHAIN AND TO PIG APOLIPOPROTEIN R.
-!- SIMILARITY: CONTAINS 6 SUSHI (SCR) REPEATS.
 DISULFID
                                                                                                                                                                                                                                           CHAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C4BPA OR C4BP
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P08607;
01-AUG-1988
                                                                                                                                                                                                                                                                                             INTERPRO; IPRO00436;
PFAM; PF00084; sushi;
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PIR; A27117; NBMSC4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                                                                                                                                                                                                                                                     tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRC
                                                                                                                                                                                                                                                                                                                                     P10998;
                                                                                                                                                                                                                                                                                 pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 08, Created)
(Rel. 28, Last sequence update)
(Rel. 35, Last annotation update)
PROTEIN PRECURSOR (C4BP).
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C4B-BINDING PROTEIN.
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SUSHI 2.
SUSHI 2.
SUSHI 3.
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SUSHI 5.
SUSHI 6.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                 Glycoprotein; Repeat; Sushi;
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protein, a reg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                       MEDLINE; 91010789.

Molina H., Kinoshita T., Inoue K., Carel J.C., Holers V.M.;

"A molecular and immunochemical characterization of mouse CR2.

Evidence for a single gene model of mouse complement receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CR2_MOUSE STANDARD; PRT; 1025 AA.
P19070;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR).
CR2.
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CARBOHYD
           SEQUENCE OF
                                                                                                                                                                               SEQUENCE OF 12-1025 FROM N.A.
                                                                                                                                                                                                                                         Fingeroth J.D.;
"Comparative structure and evolution the human C3d/EBV receptor (CD21).";
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=BALB/C;
                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
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                                                   Immunol. 145:2974-2983(1990).
                                                                                                                                                                                                                         Immuno1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGSG-WNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KTVPVWSSSPPTCEKIICSQPNILHGVIVSGYKATYTHRDSVRLACLNGTVLRGRHVIEC
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           343-401 AND 991-1025 FROM N.A.
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      THE TERM TO THE TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOCYTES ACTIVATION.

1. SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN

1. TISSUE SPECIFICITY: B LYMPHOCYTES.

1. SIMILARITY: TO HUMAN C3D/EBV RECEPTOR (CD21).

1. SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Murine complement receptor gene family characterization of the murine homolog molecular linkage to Crry ";
J. Immunol. 143:2058-2067(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fingeroth J.D., Benedict M.A., Levy D.N., Strominger J.L.; "Identification of murine complement receptor type 2."; Proc. Natl. Acad. Sci. U.S.A. 86:242-246(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kurtz C.B., Paul M.S.,
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DEGFYLLGEKSL-QCVNDSKGHGSWSGPPPQCLQSSPLTHCPDPEVKHG
                         KNGFYPATRSPVSKCTIT-----GWI-PAPRC----SLKPCDFPQFKHGRLYYEESRRPY
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                                                                                                                                      QYKCKQGFVYKERGDAVCTGSG-WNPQ-----PSCEEM--
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N-LINKED (GLCNAC...
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S -> T (IN REF. 2)
P -> A (IN REF. 2)
MISSING (IN REF. 4).
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Pred. No. 5.5e
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P20023;
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Weis J.J.
            EMBL;
                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).

1- FUNCTION: RECEPTOR FOR COMPLEMENT C3D AND FOR THE EPSTEIN-BARR VIRUS ON HUMAN B-CELLS. PARTICIPATES IN B LYMPHOCYTES ACTIVATIC ...

1- TISSUE SPECIFICITY: MATURE B LYMPHOCYTES AND FOLLICULAR DENDRIFIC CELLS OF THE SPLEEN.

1- SIMILARITY: TO MOUSE CR2. CD21 IS A MEMBER OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA) FAMILY.

1- SIMILARITY: CONTAINS 15 SUSHI (SCR) REPEATS.

1- DATABASE: NAME=PROW; NOTE=CD guide CD21 entry; WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROW/CD/CD21.HTM".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)
                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                               Weis J.J., Fearon D.T., Klickstein L.B., Wong de Bruyn Kops A., Smith J.A., Weis J.H.; "Identification of a partial cDNA clone for the virus receptor of human B lymphocytes: homolog fragments C3b and C4b of the third and fourth
                                                                                                                                                                                   entities requires a or send an email to
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                                                                                                                                                                                                       European Bioinformatics Institute. The by non-profit institutions as long thied and this statement is not removed.
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ryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
alia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a sen the Swiss Institute of Bioinformatics and the EMBI
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license@isb-sib.ch).
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                                         Biochemistry 29:11195-11209(1990).
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MIM; 134580;
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SUBUNIT: TETRAMER OF TWO A CHAINS AND TWO B CHAINS.
DISEASE: A DEFICIENCY IN FA13 CAN RESULT IN A LIFELONG BL
TENDENCY, DEFECTIVE WOUND HEALING, AND HABITUAL ABORTION.
SIMILARITY: CONTAINS 10 SUSHI (SCR) REPEATS.
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BUT IS THOUGHT TO STABILIZE THE A SUBUNITS AND
OF TRANSGLUTAMINASE FORMATION BY THROMBIN.
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A36397; A36397.
S09980; S09980.
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M14057; AAA88042.1; -.
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      , McMullen B.A., Fujikawa K., Davie E.W.; sequence of the b subunit of human factor XIII, a ten repetitive segments."; y 25:4633-4638(1986).
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COAGULATION
                                                 Mus musculus (Mouse Eukaryota; Metazoa;
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Q07968;
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                                                                      F13B OR CF13B.
                                         Eutheria;
                                        s (Mouse).
s (Mouse).
chordata;
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(Rel. 31, Last sequence update)
(Rel. 39, Last annotation update)
FACTOR XIII B CHAIN PRECURSOR (EC
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         TISSUE-LIVER;
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CHAIN) (TRANSGLUTAMINASE B
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"Molecular cloning of the b subunit of mouse coagulation factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through
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BY SIMILARITY.
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01-JUN-1994 (Rel. 2
15-JUL-1998 (Rel. 2
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01-JUN-1994 (Rel. 29, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36).
                                                                                                                                                                                                                                                                                                                                                                                                                              "Molecular cloning of a human serum protein st
complement factor H.";
J. Biol. Chem. 266:12015-12020(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HFL1
                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Estaller C., Koistinen V., Schwaeble W., Dierich M.P., Weiss E.H.; "Cloning of the 1.4-kb mRNA species of human complement factor H reveals a novel member of the short consensus repeat family related to the carboxy terminal of the classical 150-kDa molecule.";
                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4-330 FROM N.A. MEDLINE; 91268081.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                             -1- TISSUE SPECIFICITY: LIVER.
-1- SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS
-1- SIMILARITY: STRONG, TO FACTOR H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Skerka C.,
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Best Local S
Matches 51
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Kotwal G.J., Moss B.;

"Vaccinia virus encodes a secretory polypeptide structurally related
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P10998;
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MEDLINE; 89073756.

Kotwal G.J., Moss B.;

"Analysis of a large cluster of nonessential vaccinia virus terminal transposition mutant. Virology 167:524-537(1988).
                                                                                                                                                                                                 01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
COMPLEMENT CONTROL PROTEIN PRECURSOR (VCP) (SECRETORY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP; P08603; 1HFI MIM; 134371; -.
                                                       STRAIN-WR;
                                                              SEQUENCE FROM N.A.
                                                                                  Nature
                                                                                                                               STRAIN-WR;
                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                         Orthopoxvirus.
                                                                                                                                                                 Viruses; dsDNA
                                                                                                                                                                          Vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A40455; A40455.
PIR; S14604; S14604.
                                                                                                                                                                                            (PROTEIN C3) (28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                    367
                                                                                                                                                                                                                                                                                               83 CLRLCFFPFVENGHSESSGQTHLEGDTVQIICNTGYRLQNNENNISCVERGWSTPPKC 140
                                                                                                                                                                                                                                                                                                                                      23
                                                                                complement control pro
ture 335:176-178(1988).
                                                                                                                                                                                                                                                                                                            CLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKC 424
                                                                                                                                                                                                                                                                                                                                   CDFPKINHGILYDEEKYKPFSQVPTGEVFYYSCEYNFVSPSKSFWTRITCTEEGWSPTPK 82
                                                                                                                                                                                                                                                                                                                                                     CDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVP 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M65292; AAA35946.1;
M65293; AAA35947.1;
X56209; CAA39666.1;
                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycoprotein;
                                                                                                                    88318974
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                                                                                                                                                               (strain WR), and Vaccinia virus (struses, no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                             KDA PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           shi; 5.
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37661 MW;
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                                                                                                                                                                                                                                                                                                                                                                                 12.8%;
                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                         and Vaccinia virus (strain Copenhagen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUSHI
                                                                                                                                                                                                                                                                                                                                                                                 Score 315; DB 1
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IHSUS
IHSUS
IHSUS
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T -> N (IN REF. 2).
8DC0D3F92A85E035 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPLEMENT FACTOR H-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /FTId=VAR_001981.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR_001980.
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                                                                                                                                                                                                                                                  263
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                                                                                                                                                                                                                                                                                                                                                                                        DB_1; Length 330
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                                                                                                                                                                Chordopoxvirinae;
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                           deleted
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                                                                                                                                                                                                                                                                                   modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                CHAIN
                                                                                                                                                                                                PDB; 1VVC; 03-DEC-97.
PDB; 1VVD; 03-DEC-97.
PDB; 1VVE; 03-DEC-97.
                                                                                                                                                                                                                                EMBL; X13166; CAA31564.1;
EMBL; M22812; AAA69605.1;
EMBL; M35027; AAA47997.1;
PIR; A31005; WMVZSP.
                                                                                                                            REPEAT
                                                                                                                                       DOMAIN
                                                                                                                                                                               PFAM;
                                                                                                                                                                                                                                                                                                                     use
                                                                                                                                                                                                                                                                                                                                                                                                                                              "NMR studies of a viral protein that mimics the regulators complement activation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antibody-dependent complement-enhanced neutralization
and contributes to virulence.";
                                                                                                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                           <del>-</del>;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barlow P.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiles A.P., Shaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRUCTURE BY NMR OF 146-263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goebel S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPLETE GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goebel S.J., Johnson G.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                          INTERPRO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Vaccinia virus complement-control protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Virology 179:517-563(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoletti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-COPENHAGEN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              saacs S.N.,
                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: SERVES TO PROTECT THE VIRUS AGAINST COMPLEMENT ATTACK BY INHIBITING BOTH CLASSICAL AND ALTERNATIVE PATHWAYS OF COMPLEMENT ACTIVATION. BINDS C3B AND C4B.

SIMILARITY: BELONGS TO THE SUPERFAMILY OF THE REGULATORS OF COMPLEMENT ACTIVATION (RCA).

SIMILARITY: CONTAINS 4 SUSHI (SCR) REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                          MOL. Biol. 272:253-265(1997). FUNCTION: SERVES TO PROTECT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete DNA sequence of vaccinia virus."; logy 179:247-266(1990).
                                                                                                                                                                              PF00084; sushi; 4.
                                                                                                                                                                  Repeat;
                                                                                                                                                                                                                                                                                                                     non-profit
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                                                                                                                                                        Sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.,
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82
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                                                                                                                                                                                                                                                                                                                    institutions as long as its content
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                                                                                                                                                                    3D-structure.
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BY SIMILARITY.
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                                                                                              SUSHI 4.
                                                                                                                                               COMPLEMENT CONTROL PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perczel A., Campbell I.D.,
                                                                                                                                   SUSHI (SCR) REPEATS
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  CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Weller "Clonin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-OT-2000 (Rel. 40, Last annotation update)
p-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 140) (GMP-140) (PAD (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 3) (LECAM3).
                  EMBL;
                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE; 92345617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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01-APR-1993
      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Blood 80:795-800(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sanders W.E. Jr., Wilson R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SELP OR GRMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEM3_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211 ISNG---YLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                loning
                                                                                                                                                                                                SIMILARITY: TO OTHER SELECTINS/LECAMS.
SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
SIMILARITY: CONTAINS 8 SUSHI (SCR) REPEATS; MOUSE P-LECTIN LACKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ler A., Isenmann S., Vestweber D.; onling of the mouse endothelial selectins. Expression of both oring of the mouse by tumor necrosis factor alpha."; Biol. Chem. 267:15176-15183(1992).
                                                                                                                                                                                                                                                                                                                                   SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. TISSUE SPECIFICITY: STORED IN THE ALPHA-GRANULES OF PLATELETS
                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: CA(2+)-DEPENDENT RECEPTOR FOR MYELOID CELLS THAT B. TO CARBOHYDRATES ON NEUTROPHILS AND MONOCYTES. MEDIATES THE INTERACTION OF ACTIVATED ENDOTHELIAL CELLS OR PLATELETS WITH LEUKOCYTES. THE LIGAND RECOGNIZED IS SIALYL-LEWIS X.
                                                                                                                                                                                                                                                                    THE CELL SURFACE.
INDUCTION: BY TUMOR NECROSIS FACTOR ALPHA.
                                                                                                                                                                                                                                                                                                                       AND
                                                                                                                                                                                                                                                                                                 ACTIVATION BY AGONISTS, P-SELECTIN IS TRANSPORTED RAPIDLY TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VENGDGIYL----KPVYKENERFQYKCKQGFVYKERGDAVCT-GSGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YSEGTQATYKCRPGYR--TLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R-----HNGYEDFYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-DPPTCQIVKCPHPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIVSGAAEPDQEYYF-GQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGG-VDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPSISNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFNQ---CIKRRCPSPRDIDNG--QLD
      M72332;
                       M87861;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        80;
                                                                                                                                                                                    HUMAN SUSHI-2 EQUIVALENT.
                                                                                                                                                                                                                                                                                                                     WEIBEL-PALADE BODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92340571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Mouse)
      AAA40008.1;
AAA37712.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
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                                                                                                                                                                                                                                                                                                                       OF ENDOTHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Ver
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ballantyne C.M., Beaudet A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of in
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MGD; MGI:98280; SELF.
INTERPRO; IPRO00561; -.
INTERPRO; IPRO01304; -.
INTERPRO; IPRO02396; -.
                                                                            Query Match
Best Local
                                                      Matches
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PFAM; PF00059; lectin_c; 1.
PFAM; PF00084; Sushi; 8.
PRINTS; PR00343; SELECTIN.
PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; 1
PROSITE; PS01186; EGF_2; 1
PROSITE; PS01615; C_TYPE_LECTIN_1; 1
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HSSP; P16109; 1FSB.
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1 EDCKGPPPRENSEILSGSWSEQ------LYSEGTQATYKCRPG--YRTLGTIVKVCK 49
                                                                               Similarity
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                                                                            12.7%;
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                                                                                                                                                                                        MW;
                                                      60;
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SUSHI 1.
SUSHI 2.
SUSHI 3.
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SUSHI 6.
SUSHI 6.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 7.
SUSHI 8.
BY SIMILARITY.
                                                    Score 310.5;
Pred. No. 2.3e
60; Mismatches
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E5173074D2F66E68 CRC64;
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                                                                                                                                                                                                                                                                     (BY SIMILARITY)
                                                                               .3e-16;
                                                                                                                                                                                                                                      SIGNAL (PROBABLE).
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                                                         Indels
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                                                         91;
                                                      Gaps
                                                         30;
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IF-APEQGNLDCSHVHGEFGVGSICHFSCNEDFEL-LGSENVECTVSGRWSAPPPTC 567		513	ğ
IFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENG-WS-PPPKC 424		372	γ
NGSMTCVQFLGNSTYKSTCQFMCDEGFYLSGPERLDCSPSGHWTGTPPTCEAIKCPG 512		456	Б
SRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG-WEPEVPCLRQC 371		322	¥
S-VIRCLATGHWNGAPPECQAVSCAPMLSPE 455	GTLTYQSVCSFSCDEGSLLVGAS-V	404	ğ
-RYECKNGFYPATRSPVSKCTITG-WIPA-PRCSLKPCDFPQFKHGRLYYEE 321	1	273	Ϋ́
CTFLCAEGFVLKGNDAIQCADSGQWTAPAPFCEALQCPEFPVPSKAQVNCSDPF 403	O CTFLCAEGFVLKGNDAIQCADSGQWTAPAPFCEALQC	350	ğ
FQYKCKQGFVYKERGDAVCTGSG-WN-PQDSCEEMTCLTPYIANGIYTPHRIKHRIDDEI 272		215	γ
FECQPGYRARGSNTLHCTGSGQWSEPLPTCEAIACEPPEIPIHGSMDCVPSTGTFGYNSS 349		290	B
FECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPPRVENGDGIYLKPVYKENER 214		158	ž
GYELDGPGEL-QCLASGIWTNNPPKCDAVQCQSLEAPPHGTMACMHPIAAFAYDSSCK 289		233	Ф
GYQLLGEIDYRECDADG-WTNDIPICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVR 157		99	δĀ
VLMNCSHP	PGFYGPECEYVKECGKVNIPQHVLMNCSHP	187	₽
NGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDE 98	0 NGEWVPSNPSRICRKRPCGHPGDTPF	50	ΩV

Search completed: November 21, 2000, 16:49:28 Job time: 331 sec

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Maximum Match 100%
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SPTREMBL_14:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb:
6: sp_manmal:*
7: sp_mhc:*
8: sp_organelle
9: sp_plant:*
10: sp_plant:*
11: sp_rodent:*
12: sp_vrius:*
13: sp_vertebra:
14: sp_unclassi
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Gapop 10.0 , Gapext 0.5
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1 EDCKGPPPRENSEILSGSWS......DTYYCTENGWSPPPKCVRIK 428
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             sp_plant:*
sp_rodent:*
sp_virus:*
sp_vertebrate:*
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sp_mammal:*
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sp_unclassified:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

RM SEQUENCE OF 1-9 FROM N.A. RA DOMINGUEZ O.; RL Thesis (1993), Inmunologia, Hospital Trias I Pujol, DR EMBL; X07523; CAA30403.1; DR EMBL; W1283; AAA52013.1; DR EMBL; U56979; AAB01987.1; DR EMBL; 29665; CAA82763.1; DR HSSP; P10998; IVVC. DR INTERPRO; IPR000436; DR PFAM; PF00084; Sushi; 7. KW Signal. 1 18 POTENTIAL.	DIENCE OF 226-449 FROM N.A. Stensen T., Wetsel R.A., Tack B.F.; ructural analysis of human complement prote dding protein, beta 2-glycoprotein I, and th Immunol. 136:3407-3411(1986). UENCE OF 1-19 FROM N.A. D.P., Williams S.A.; mitted (APR-1996) to the EMBL/GenBank/DDBJ		PRT; 449 ireated) ast sequences ast annotate.
jol, Spain.	e Ba fragment of B2.";	idae; Homo. lidae; Homo.	•

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RESULT
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Best Local Similarity
Matches 206;
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SEQUENCE
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                 Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                   01-NOV-1996 (TREMBLrel. 01, Created)
01-NOV-1996 (TREMBLrel. 01, Last sequence update)
01-MAY-2000 (TREMBLrel. 13, Last annotation update)
CCP MODULES 3-12, WITH PARTS OF CCP 2 AND 13 (FRAGMENT).
                                                                                                          Soames C.J., Day A.J., Sim R.B.;
"Prediction from sequence comparisons of residues of factor H involved in the interaction with complement component C3b.";
Biochem. J. 315:523-531(1996).
EMBL; X98697; CAA67257.1; -.
HSSP; P10998; 1VC.
                                                                                                                                                                                                                                                                                                               Q28085;
                                                                                                                                                                                                                                                                                                                           Q28085
                                                                                      PFAM; PF00084; sushi; 11.
                                                                                                                                                                                                                         Bovidae; Bovinae; Bos.
                                                                                                                                                                             MEDLINE; 96202005.
                                                                                                                                                                                         TISSUE-LIVER;
                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                     PPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNEKPQCVEISCLPPRVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PICEVVKCLPVTELENGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSP 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \texttt{LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITGWIPAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW
                                                                                                                                                                                                                                                                                                                                                                                                                            WSPAVPCLRKCYFPYLENGYNQNYGRKFVQGKSIDVACHPGYALPKAQTTVTCMENGWSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RCTLKPCDYPDIKHGGLYHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWDHIHCTQDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            288;
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449 /
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 Conservative
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                                                        ΑA;
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51033 MW;
                                                      669
75683 MW;
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         50.6%;
57;
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Pred. No. 3.3e-142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
; C2AAD47F155343E3 CRC64;
Score 1242; DB
Pred. No. 9.7e-1
7; Mismatches
                                                                                                                                                                                                                                                                                                                           PRT;
                                                        D0D9DB30EE747AC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                            669 AA
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            DB 6;
7e-101;
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Matches
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-1990) to the EMBL/GenBank/DDBJ databases EMBL; M29010; AAA37415.1; -. HSSP; P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vik D.P., Mun
Chaplin D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chaplin D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vik D.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERPRO; IPR000436; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
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                                                                                                                                                                                                                                            236 SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG 295
416 NGWSPPPKCVRIK 428
                                           135
                                                                                      356
                                                                                                                                                      296 WIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLR 355
                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                               75 WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYRCDNGFSPPSGYSWDYLR 134
                                                                                                                                                                                                                      15 TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHRSDDEIRYECNYGFYPVTGSTVSKCTPTG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biol. Chem. 0:0-0(0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGHNOHREEKYLOGETVRVHCYEGYSLONDQNTMTCTESGWSPPPRCIRVK 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDADGWTNDIPICEVVKCLPVTELE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \tt NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP
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                                                                  CTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTE 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RLYY--SYRGYFPARVNQQFVYSCDHHFVPPSQRSWDHLACTAEGWSPEEPCLRQCIFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNGWEPEVPCLRQCIFHY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RVENGDGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTGSGWNPQPSCEEMTCLTPYIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGRIVSGAAEPDQEYYFGQVVRFECNSGFKIEGQKEMHCSENGLWSNEKPQCVEISCLPP 195
                                           CTAQGWEPEVPCVRKCVFHYVENGDSAYWEKIYVQGQSLKVQCYNGYSLQNGQDIMTCTE
                                                                                                                                                                                                                                                                                                        al Similarity
137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                PF00084; sushi;
NCE 452 AA; 5:
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                   51602 MW;
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71.0%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                        Score 813; DB 11;
Pred. No. 2.3e-63;
8; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                     2B697A4FFC6E13CA CRC64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
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195

NGWSPPPKCIRIK

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Best Local S
Matches 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification and sequence analysis of related transcripts in mouse liver.";
J. Biol. Chem. 265:3193-33201(1990).
EMBL; M29007; AAA37413.1; -.
HYSEP; P10998; IVVC.
INTERPRO; IPRO00436; -.
PFAM; PF00084; Sushi; 4.
SEQUENCE 303 AA; 34498 MW; 51C66E509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              061405

061405;

01-NOV-1996 (TremBLrel. 01,

01-NOV-1996 (TremBLrel. 01,

01-MAY-2000 (TremBLrel. 13,
                                                                                                                                                                                                                                                     Q91275
Q91275;
                                                                                                                                                               COMPLEMENT REGULATORY PLASMA PROTEIN.

Paralabrax nebulifer (barred sand bass).

Bukaryota, Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Acanthopterygii;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                 01-NOV-1996 (TREMBLIEGL 01, 01-NOV-1996 (TREMBLIEGL 01, 01-MAY-2000 (TREMBLIEGL 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chaplin D.D.
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             neblifer).";
Biochem. J. 301:391-397(1994).
EMBL; L21703; AAA92556.1;
HSSP; P08603; 1HFH.
                                                                                                               TISSUE-LIVER;
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE; 90153969
                                                             complement-regulatory plasma
                                                                         Dahmen A., Kaidoh T., Zipfel P.F., Gigli I.;
"Cloning and characterization of a cDNA representing
                                                                                                     MEDLINE;
                                                                                                                                                     Percomorpha;
                                                                                                                                                                                                                                                                                                                                                        416
                                                                                                                                                                                                                                                                                                                                                                                 135
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Local Similarity 70.8%;
nes 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAWLSTAKGEEKTCSPPYILNGIYTPHRIIHKSDDEIRYECNYGFYPVTGSTVSKCTPTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGWNPQPSCEEMTCLTPYIPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG
                                                                                                                                                                                                                                                                                                                                                                                             CTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYYCTE
                                                                                                                                                                                                                                                                                                                                                                                                                                   WIPVPRCTLKPCEFPQFKYGRLYYEESLRPNFPVSIGNKYSYKCDNGFSPPSGYSWDYLR
                                                                                                                                                                                                                                                                                                                                NGWSPPPKCIRI
                                                                                                                                                                                                                                                                                                                                                        NGWSPPPKCVRI 427
                                                                                                                                                                                                                                                                                                                                                                                 CTAQGWEPEVPCVRKCVFHYVENGDSTYWEKIYVQGQSLKVQCYNGYSLQNGQDTMTCTE
                                                                                                   94318039.
  IPR000436;
                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                       Perciformes;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kozono H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 811; DB Pred. No. 2.2e
                                                                                                                                                                                                                                           Created)
                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51C66E50906F4C24 CRC64;
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                                                                                                                                                     Serranidae;
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                                                                sand
                                                                                                                                                       Paralabrax.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murinae;
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SEQUENCE 1053 AA; 117597 MW;
     PFAM; PF00084;
SEQUENCE 808
                                                                                                                                                                                                     MEDLINE; 90153969.
Vik D.P., Munoz-Canoves
Chaplin D.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q61408
  INTERPRO; IPR000436; -. PFAM; PF00084; sushi; 13 SEQUENCE 808 AA; 9165
                                                                               EMBL; M29009; AAA37416.1; HSSP; P08603; 1HCC.
                                                                                                                              related transcripts in mouse liver. J. Biol. Chem. 265:3193-3201(1990).
                                                                                                                                                                                                                                                                                                                                                                                                              COMPLEMENT FACTOR H-RELATED
                                                                                                                                                                                   "Identification and
                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   561
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                                                                                                                                                                                                                                                                                                                                    Eutheria;
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                                                                                                                                                      in mouse liver.";
                                                                                                                                                                                                                                                                                                                                    Rodentia;
                                                                                                                                                                                                                                                                                                                                                              Chordata;
     91654 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      01, Created)01, Last sequence update)13, Last annotation updat
                                                                                                                                                                                                                                P., Kozono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN.
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Pred. No. 1.4e-41;
                                                                                                                                                                                                                                                                                                                                    Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
       6FD97D53CE74DF6D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
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                                                                                                                                                                                                                                  L.G.,
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                                                             Q63135;
Q1-NOV-1996 (TremBLrel. 01, Created)
Q1-NOV-1996 (TremBLrel. 01, Last sequence update)
Q1-MAY-2000 (TremBLrel. 13, Last annotation update)
COMPLEMENT REGULATORY PROTEIN.
 SEQUENCE FROM N.A
                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                     Rattus norvegicus (Rat).
                                                                                                                                                  Q63135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TYEMBLYE1. 13, Created)
01-MAY-2000 (TYEMBLYE1. 13, Last sequence update)
01-JUN-2000 (TYEMBLYE1. 14, Last annotation update)
01-JUN-2000 (TYEMBLYE1. 14, Last annotation update)
01-JUN-2000 (TYEMBLYE1. 14, Last annotation update)
01-JUN-2000 (TYEMBLYE1. 13, Created)
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01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DJ15D12.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                            293 ITGWIPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWD 352
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                                                                                                                                                                                                                   CTEKGWSPTPRCIRVR 144
                                                                                                                                                                                                                                             CTENGWSPPPKCVRIK 428
                                                                                                                                                                                                                                                                                                YLRCTVNGWEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQDTYY 412
                                                                                                                                                                                                                                                                                                                             LTLWVSCANGQVKPCDFPDIKHGGLFHENMRRPYFPVAVGKYYSYYCDEHFETPSGSYWD 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLFWDYLRCTVQGWKPEVPCVRKCVFHYVENGEFAYWEKIYVQGQSLKVQCYNGYSLQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LSNILLTAWLSTAKGEVKSCEFPQFKYGRLYFEEILRPNFPVSIGNKYSYKCDNGFSPPS 68
                                                                                                                                                                                                                                                                        YIHCTQNGWSPAVPCLRKCYFPYLENGYNQNYGRKFVQGNSTEVACHPGYGLPKAQTTVT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDTMTCTENGWSPPPKCIRIK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF00084;
NCE 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91;
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                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      sushi;
AA; 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.1%; 64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      37323 MW;
                                                                                                                                                                                                                                                                                                                                                                                                 19.5%;
55.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                 Score 478; DB 4;
Pred. No. 3.6e-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 566; DB 11;
Pred. No. 2.1e-41;
""ematches 27;
                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      67B64121D71CD65F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                  559 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 AA
                                                                                                                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                              Length 330;
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                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                          099254 PRELIMINARY; PRT; 679 AA.
099254:
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                   COMPLEMENT RECEPTOR TYPE 2
Kurtz C.B., O'Toole
                                 STRAIN=BALB/C
                                                 SEQUENCE FROM N.A.
                                                                                                  Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERPRO; IPRO00436; -. PFAM; PF00084; sushi; 7 SEQUENCE 559 AA; 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Dohi N., Sakurada C., Nonaka M., Okada N., Oka
Submitted (CCT-1997) to the EMBL/GenBank/DDBJ
EMBL; L36532; AAA91821.1; -.
EMBL; D42115; BAA22548.1; -.
HSSP; P10998; IVVC.
                 MEDLINE; 90229754
                                                                                  Mammalia; Eutheria;
                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quigg R.J., Lo C.F., Alexander J.J., Sneed A.E., Moxley G. III; "Molecular characterization of rat Crry: widespread distribution two alternative forms of Crry mRNA.";
                                                                                                                                                                                                                                                                                                                      438
                                                                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                      388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 AEAPICESIPCEIPPSIPNGDFFS----PNREDFHYGMVVTYQCNTDARGKKLFNLVGEP 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 NDIPICEVVKCLPVTELENGRIVSGAAEPDQE-YYFGQVVRFECNSG-----FKIEGQK 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93 VCIRKQCETPLDPQNGI--VHVNTDIRFGSSITYTCNEGYRLIGSSSAMCIISDQSVAWD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 CPAPPLFPYAKPINPT-DESTFPVGTSLKYECRPGYIKRQFSITCEV--NSVW--TSPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CKGPPPRENSEILSGSWSEQLYSEGTQATYKCRPGY--RTLGTIVKVCKNGEWVPSNPSR
                                                                                                                                                                                                                                                                       ٥
                                                                                                                                                                                                                                                                                                                                                  YIEGQSAKVQCHSGYSLPNGQDTYYCTENGWSPP-PKCV 425
                                                                                                                                                                                                                                                                                                                                                                                     NVALECEDGYTLEGSS----QSQCQSDASwDPPLPKCVSQVICKLPQDMSGFQKGLQMKKD
                                                                                                                                                                                                                                                                                                                   YYYGDNVALECEDGYTLEGSSQSQCQSDASWDPPLPKCV 476
                                                                                                                                                                                                                                                                                                                                                                                                                     EYSYYCDNGFTTPSQSYWDYLRCTVN-GWEPEVP-CLRQCIFHYVE----YGESSYWQRR 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-YQLKGNSSSHCVLDGVESIWNSSVPVCEQVICKLPQDMSGFQKGLQMKKDYY---YGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIHCTSIDGQVGVWSGPPPQCIELNKCTPPHYENAVIVSKNKSLFSLRDMVEFRCQDGFM 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMHCS----ENGLWSNEKPQCVEIS-CLPPRVENGDGIYL-KPVYKENERFQYKCKQGFV 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GFYPATRSPVSKCTITG----W-IPAPRCSLKPCDFPQFKHGRLYYEESRRPYFPVPIGK 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      \tt MKGDSSVYCRSLNRWEPQLPSCFKVKSCGAFLGELPNGHVFVPQNL--QLGAKVTFVCNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YKERGDAVCTG-SGWNPQ-PSCEEMTCLTPY---IPNG-IYTPHRIKHRIDDEIRYECKN 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ICRKRPCGHPGDTPFGSFRLAVGSEFEFGAKVVYTCDEGYQLLGEIDYRECDAD----GWT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                  Metazoa;
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                                                                                  Rodentia;
                                                                                                Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.0%; Score 466; DB 11; 26.6%; Pred. No. 7.6e-33;
Christensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91; Mismatches 190;
                                                                                                                                               (CR2) (FRAGMENT).
                                                                               Sciurognathi;
                                                                                                  Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29E10F6A21DB9B6E CRC64;
S.M.,
Weis
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                                                                                Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             databases
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RESULT
Q28769
ID Q2
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DT 01
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Best Local S
Matches 126
          Q28769;
Q28769;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 21-367 FROM N.A. MEDLINE; 95105691.
Kim Y.U., Kinoshita T., Molina H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The murine complement receptor gene family. IV. Alternative splicing of Cr2 gene transcripts predicts two distinct gene products that share homologous domains with both human CR2 and CR1."; J. Immunol. 144:3581-3591(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Exp. Med. 181:151-159(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mechanisms of both
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COMPLEMENT RECEPTOR (FRAGMENT).
                                                                                                                                               438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 YSEGTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVG
                                                                                                  10
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U17123 AAA78271.1;

U17124 AAA78271.1;

U17125 AAA78271.1;

U17126 AAA78271.1;

U17126 AAA78271.1;

U17127 AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;

AAA78271.1;
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                                                                                                                                             AIFCISENQVHATWDKAPPIC 458
                                                                                                                                                                                                                                                              CEVKSCDAIPNHLLHGRVFLPPN-----LQLGAEVSFVCDLGFQLKGKPSS-----
                                                                                                                                                                                                                                                                                                                                                                              VKCPMPEIENGLVESG--FKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPPLPTC
                                                                                                                                                                                                                                                                                                                                                                                                                                        SSSRD---SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPPPQCIPR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGAAEPDQEYYFGQVVRFECNSG----FKIEGQKEMHCSEN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --IEFGSTITYSCNQGYRLIGDSSATCIVSDNTVMWDNDMPLCESIPCESPPAISNGDFY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEFEFGAKVVYTCDEGYQLLGEIDYRECDADG----WINDIPICEVVKCLPVTELENGRIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSVHINTG
                                                                                                                                                                        TYYC-TEN----GW-SPPPKC 424
                                                                                                                                                                                                    IPEGETVIWNNKFPVCEQISCDPPPEVKNARKPYYSLPIVPGTVLRYTCSPSYRL-IGEK
                                                                                                                                                                                                                                 TVNG----WEPEVPCLRQCIFH---YVEYGESSYWQRRYIEGQSAKVQCHSGYSLPNGQD 409
                                                                                                                                                                                                                                                                                        CSLKPCD-FP-QFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFT---TPSQSYWDYLRC 356
                                                                                                                                                                                                                                                                                                                     - {\tt FMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNTVPT}
                                                                                                                                                                                                                                                                                                                                                EEMTCLTPY-IPNGIYTPHRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WI-PAPR 301
                                                                                                                                                                                                                                                                                                                                                                                                        ISCLPPRVENG----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVC-TGSGWNPQ-PSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement regulatory protein Crry/p65 uses the isms of both human decay-accelerating factor and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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             (TrEMBLrel. 01, (TrEMBLrel. 01, (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74916 MW;
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            Last sequence update)
Last annotation updat
                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 453; DB 11
Pred. No. 1.3e-31
3; Mismatches 17
                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52FC00FDCED20CDC CRC64;
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                                                                       522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GLWSNEKPQCV-E
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RESULT
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Best Loc
Matches
                                                                                                                                                      Q29530 PRELIMINARY; PRT; 2014 AA. Q29530; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation updat COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birmingham D.J., Logar C.M., Shen X.P., Chen W. Submitted (MAY-1996) to the EMBL/GenBank/DDBJ EMBL; L7797; AA89004.1; -. HSSP: P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PFAM; PF00084; sushi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=BONE MARROW;
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erythrocytes.";
            MEDLINE; 94292799.

Birmingham D.J., Shen X.P., Hourcade D., Nickells M.W., Atkinson J.P. Birmingham D.J., Shen alternatively spliced form of CR1. Candidate for the 75,000 M(r) complement receptor expressed on chimpanzee
                                                                                                                Eukaryota;
                                                                                                                              Pan troglodytes (Chimpanzee).
                                                                      SEQUENCE FROM N.A.
                                                                                                   Mammalia;
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                                                                                                                                                                                                                                                                                                     GMTVNLIGESTIRCTSDPQGNGVWSSPAPRC
                                                                                                                                                                                                                                                                                                                                                            MKALWNSSVPVCEQ-IFCPNPPAILNGRHIGAPLGDIPY-----GKEVSYICDPHPDR
                                                                                                                                                                                                                                                                                                                                                                                         ----WEPEVPCLRQCIF-----HY-VEYGESSYWQRRYIEGQSAKVQC--HSGY
                                                                                                                                                                                                                                                                                                                                                                                                                   KSCDDFLGQLPHGRV-----LFPLNLQLGAKVSFVCDEGFRLKGRF---ASHCVLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                               KPCD--FPQFKHGRLYYEESRRPYFP--VPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VCQPPPEILHGEHTPSHQDFSPGQEVFYSCEPG-YDLRGAASLHCTPQGDWNPEAPICTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134;
                                                                                                                                                                                                                                                                                                                                SLP---NGQDTYYCTE----NG-W-SPPPKC 424
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                                                                                                   Eutheria; Primates;
                                                                                                                  Metazoa;
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                                                                                                                  Chordata;
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Pred.
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                                                                                                   Catarrhini;
                                                                                                                  Craniata; Vertebrata;
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                                                                                                    Hominidae;
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                                                                                                                  Euteleostomi;
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                                                                                                                                                                                                                  Q9UQV2 PRELIMINARY; PRT; 559 AA.
Q9UQV2;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2000 (TrEMBLrel. 14, Last annotation update)
HUMAN CR1 MRNA FOR C3B/C4B RECEPTOR SECRETED FORM PRECURSOR (FRAGMENT).
            Hourcade D., Miesner D.R., Atkinson J.P., Holers V.M.;
"Identification of an alternative polyadenylation site in the human C3b/C4b receptor (complement receptor type 1) transcriptional unit and prediction of a secreted form of complement receptor type 1.*;
J. Exp. Med. 168:1255-1270(1988).
EMBL; X14362; CAA32541.1;
INTERPRO; IPR000436; -.
                                                                                                                                                           Homo sapiens (Human).
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
INTERPRO; IPR000834; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1277
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HSSP;
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PFAM; PF00084; sushi; 30.

PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_2.
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                                                                                                                                                                                                                                                                                                                                                                                                                           SGYSLP---NGQDTYYCTE----NG-W-SPPPKC 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LVGMRSLWNNSVPVCEQ-IFCPNPPAILNGRHTGTPFGDIPY-----
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P08603; 1HFI.
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89010527.
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2014 AA;
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30.2%;
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Pred. No. 1
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Best Local
Vik D.P., Wong W.W.;
Submitted (JUN-1993) to the
EMBL; L17418; AAB60694.1; J
EMBL; L17390; AAB60694.1; J
EMBL; L17391; AAB60694.1; J
EMBL; L17392; AAB60694.1; J
EMBL; L17393; AAB60694.1; J
                                                                                                                                                                                                                                                        Q16745 PRELIMINARY;
Q16745;
Q16745;
01-NOV-1996 (TrEMBLrel. 01, C
01-NOV-1996 (TrEMBLrel. 01, L
01-MAY-2000 (TREMBLREL. 13, L
COMPLEMENT RECEPTOR 1.
                                                                                                                        Vik D.P., Wong W.W.;
"Structure of the gene for the F allele of complement receptor type and sequence of the coding region unique to the S allele.";
J. Immunol. 151:6214-6224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal.
                                                                                                                                                                                                                      Mammalia;
                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                               Homo sapiens
                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                              MEDLINE; 94065175.
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                                                                                                                                                                                                                                                                                                                                                         13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRV-CQPP--PDVLHAERTQRDKDNFSPGQEVFYSCEPG-YDLRGAASMRCTPQGDWSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCLPPRVENG-----DGIYLKPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EEMTCLTPYIPNGIYTPHRIKHRID----DEIRYECKNGFYPATRSPVSKCTITG-WIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KCTPPNVENGILVSDN----RSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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AAB60694.1; JOINED.
AAB60694.1; JOINED.
AAB60694.1; JOINED.
AAB60694.1; JOINED.
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61424 .
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                                                                    to the EMBL/GenBank/DDBJ
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27.7%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                   Created)
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Pred. No. 2.6e-30
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                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi;
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                                                                 databases
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                                                                                                                                                                                                                                                                                                                                                                                                462
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ERPRO; IPR000436; -.
ERPRO; IPR000834; -.
IPR001824; -.
IERPRO; IPR001824; -.
AM; pF00084; sushi; 30.
OSITE; PS00087; SCD_CZ_N_1; UNKNOWN_1.
PS000133; CARBOXYPEPT_ZN_2; UNKNOWN_2.
PS0SITE; PS00133; CARBOXYPEPT_BN_2; UNKNOWN_2.
POSITE; PS00133; CARBOXYPEPT_N_2, UNKNOWN_2.
POSITE; PS00133; CARBOXYPEPT_N_2, UNKNOWN_2.
POSITE; PS00133; CARBOXYPEPT_N_2, UNKNOWN_2.
POSITE; PS00133; CARBOXYPEPT_N_2, UNKNOWN_2.
PS00133; CARBOXYPEPT_N_2, UNKNOWN_2.
PS00134; PS00135; UNKNOWN_1.
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                                                                ---CVLAGMESLWNSSVPVCEQ-----
                                                                                                                                                                             APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTYLNYECRPGYSGRPFSIICLKNSVWTGAKDR--CRRKSCRNPPDPVNGMVHVIKG--I 121
                                                                                                      YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN--
                                                                                                                                                APTCEVKSCDDFMGQLLNGRV-----LFPVNLQLGAKVDFVCDEGFQLKGSSASY--
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L17406;
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AAB60694.1;
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Pred. No. 1.3e-29;
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-GQDTYYCTE---
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                                                              ---IFCPSPPVIPNGR
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NG-W-SPPPKC
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INTERPRO; IPR000436; -.
INTERPRO; IPR000834; -.
INTERPRO; IPR001424; -.
INTERPRO; IPR001424; -.
PFAM; PF00084; sushi; 37.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_3.
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Q16744;
Q1-NOV-1996
Q1-NOV-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vik D.P., Wong W.W.;
Submitted (JUN-1993)
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Vik D.P., Wong W.W.;

"Structure of the gene for the F and sequence of the coding regio J. Immunol. 151:6214-6224(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   432 HTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRC
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L17390 AAB60695
L17391 AAB60695
L17392 AAB60695
L17393 AAB60695
L17393 AAB60695
L17394 AAB60695
                                                                                                                                                                                                                                                                                                                                 L17408;
L174109;
L174111;
L174121;
L174123;
L17413;
L17414;
L17416;
L17416;
L17416;
L17417;
L17419;
                                                                                                                              L17430; AAB60695
P08603; 1HFI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L17406;
L17407;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Metazoa; Chordata;
Eutheria; Primates;
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13, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Q2952B
Q2952B
ID Q2952B
AC Q2953B
DT 01-NOV
DT 01-NOV
DT 01-MAY
DT COMPLE
GN CR1.
OS Papio
OC Eukary
OC Mammal
OC Cercop
RN [1]
RP SEQUEN
RA Atkins
RL Submitt
RF PROSIT
DR PFAM,
DR PFAM,
DR PFAM,
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DR PFAM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                 Query Match 17.8%; Score 436; DB 6; Length 1911; Best Local Similarity 28.6%; Pred. No. 1.4e-29;
Matches 130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q29528;

01-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

COMPLEMENT RECEPTOR 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papio hamadryas (Hamadryas baboon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q29528
                                                                                                                                                                                                               PFAM; PF00084; Sushi; 29.

PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.

PROSITE; PS00133; CARBOXYPEPT_ZN_2; UNKNOWN_4.

NON_TER 1911 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clemenza L., Subramanian B.V., Nickells M.W., Atkinson J.P.;
                                                                                                                                                                                                                                                                                                                                                                                                 INTERPRO; IPRO00436; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                               INTERPRO; IPR001424; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432 HTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPQGNGVWSSPAPRC 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          353 YLRCTVNG----WEPEVPCLRQCIFHYVEYGESSYWQRRYIEGQSAKVQCHSGYSLPN-- 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TNRE---NFHYGSVVTYRCNPGSGGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPN 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---CVLAGMESLWNSSVPVCEQ--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APTCEVKSCDDFMGQLLNGRV------LFPVNLQLGAKVDFVCDEGFQLKGSSASY-- 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APRCSLKPCD--FPQFKHGRLYYEESRRPYFPV--PIGKEYSYYCDNGFTT--PSQSYWD 352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KCTPPNVENGILVSDN----RSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKC-LPVTELENGRIVS 141
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                                                                                                                                                                                     1911 AA;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                 210173 MW; 535A4DD0EAFA521D CRC64;
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   88;
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1241 RDRGMTFNLIGESTIRCTSDLQGNGVWSSPAPRC 1274
                                                                                                                                                                                                              1143
                                                                                                                                                                                                                                                                                                              1084 CQPPPEILHGEHTPSHQDKFSPGQEVFYSCEPG-YDLRGAASLHCTPQGDWSPEAPRCAV 1142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAEPDQEYY-FGQVVRFECNSG-----FKIEGQKEMHCSEN----GLWSNEKPQC-VEI 190
                                                                                                                                                          --WEPEVPCLRQ---------CIFHYVEYG-ESSYWQRRYIEGQSAKVQC--H 399
                                                                                                                                                                                                           KSCDDFLGQLHHGRVLVP-----FNLQLGAKVSFVCDEGFRLKGSS----VSHCVLVGMR 1193
                                                                                                                                                                                                                                                             KPCD--FPQFKHGRLYYEESRRPYFPVPIGKEYSYYCDNGFTTPSQSYWDYLRCTVNG-- 360
                                                                                                                                                                                                                                                                                                                                                                                                                       KCMPPNVENGILVSVNRSLFSLNEVVEFRCQPGFVMKGPRRVQCQALNKWEPELPSCSRV 1083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVGSRINYSCTTGHRLIGH-SSAECIISGNTAHWSTKPPICQRIPCGLPPPIANGDFIS- 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTSLKYECRPEYYGKPFSITCLDNLVW--SSPKDVCKRKSCKTPPDPVNG--MVHVITDI
                                                 SGYSLP---NGQDTYYCTE----NG-W-SPPPKC 424
                                                                                                     SLWNNSVPVCEHIFCPNPPAILNGRHTGALLGDIPYGKEISY----
                                                                                                                                                                                                                                                                                                                                                                TCLTPYIPNGIYTP-HRIKHRIDDEIRYECKNGFYPATRSPVSKCTITG-WIP-APRCSL 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SCLPPRVENGDGIYL-KPVYKENERFQYKCKQGFVYKERGDAVCTG-SGWNPQ-PSCEEM 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---TNREYFHYGSVYTYRCNLGSGRKKLFELVGEPSIYCTSKDDQVGIWSGPAPQCIIPN 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EFGAKVVYTCDEGYQLLGEIDYRECDADG----WTNDIPICEVVKCLPVTELENGRIVSG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTQATYKCRPGYRTLGTIVKVCKNGEWVPSNPSRICRKRPCGHPGDTPFGSFRLAVGSEF 86
                                                                                                              ----TCDPH 1240
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Search completed: November 21, 2000, 16:49:00 Job time: 338 sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Eur. J. Immur A;Title: Hume A;Reference r A;Accession: A;Status: not A;Molecule t; A;Note: this R;Sim, R,B.; Biochem, J.; A;Title: Puri A;Reference r A;Accession: A;Molecule t; A;Residues: I A;Residues: I Biochemistry	A; Acces A; Statu A; Molec A; Resid A; Note: R; Schul Eur. J. A; Title A; Title A; Refer A; Molec A; Molec A; Note: R; Schwal	RESULT 1 RHBHURS Complement N; Alternat C; Species: C; Date: 31 C; Accessio R; Ripoche, Biochem. Biochem: T A; Title: T A; Residues A; Cross ree A; Note: pa A; Note: pa A; Note: 40 R; Estaller B; Title: H A; Title: H	33 33 33 33 33 33 33 33 33 33 33 33 33
Eur. J. Immunol. 17, 1485-1489, 1987 A;Title: Human complement factor H: eA;Reference number: A61103; MUID:8805 A;Accession: A61103 A;Status: not compared with conceptua A;Molecule type: mRNA A;Residues: 27-76 <sc2> A;Note: this is a partial sequence of R;Slm, R.B; Disciplo, R.G. Biochem. J. 205, 285-293, 1982 A;Title: Purification and structural A;Reference number: A26505; MUID:8304 A;Accession: A26505 A;Molecule type: protein A;Residues: 19-20, 'Q',22-29,'Y',31-33 R;Barlow, P.N.; Norman, D.G.; Steinka Biochemistry 31, 3626-3634, 1992</sc2>	A;Accession: B00238 A;Accession: B00238 A;Accession: Compared w A;Molecule type: mRNA A;Residues: 1-33,434-449 A;Note: only portions of R;Schulz; T.F.; Schwaeble Eur. J. Immunol. 16, 135; A;Title: Human complement A;Reference number: A27877 A;Molecule type: mRNA A;Accession: A27877 A;Molecule type: mRNA A;Residues: 'IL',55-401 A;Note: an additional nu A;Note: an additional nu A;Note: an additional nu	nt ates: s: s	274.5 274.5 274.5 274.5 274.5 274.5 274.5 274.5 270.5 270.5 270.5 270.5
Immunol 17, 1485-1489, 1987 : Human complement factor H: exence number: A61103; MUID:88055 sion: A61103 s: not compared with conceptual ule type: mRNA ules: 27-76 <sc2> this is a partial sequence of this is a partial sequence of R.B.: Discipio, R.G. y 205, 285-293, 1982 : Purification and structural sence number: A2505; MUID:83048 sion: A25505 ule type: protein ule type: protein y, P.N.; Norman, D.G.; Steinkas sistry 31, 3626-3634, 1992</sc2>	B60238 B60238 t compared w t compared w poer mana 1-33,434-449 portions of F; Schwaebl nol. 16, 135 nol. 16, 135 nol nomplemen number: A278 A2787 ype: mRNA '11',55-401, dditional nu dditional nu	factor H precursor, names: complement Homo sapiens (man) Dec-193 #sequence, 18 803013; B60238; A J; Day, A.J; Harr 249, 593-602, 1988 e complete amino ac number: S00254; MU 1-449: EMBL: X0752 t of this sequence, -Tyr was also found	1114444444 111444444444444444444444444
## 1485-1489, 19 ant factor H 11103; MUID:8 mUID:8 with concep kal sequence R.G. 33, 1982 and structur 5505; MUID:8 ln L2-29,'V',31	cESTV this 1. e, W.; S 1-1355, 1-1355, 1-1364, 177; MUIE 77; MUIE 77; MUIE	precursor, sens (ma) when the gens (ma) when the ge	349 2 349 2 377 2 376 2 366 2 2 366 2 2 360 2 1 300 2 1
1489, 1987 [Eactor H: expression of the expressi	eptual t kiloba kiloba ttanley, 1986 :8705420 :8705420 :8705420 :8705420	precursor, short splice ficens (man) tesquence_revision 23-Feb; B60238; A27877; A61103; AJ.; Harris, T.J.R.; Sim 3-602, 1988 te amino acid sequence of s00254; MUID:88134059 NA RRIPS EMBL:X07523; EMBL:Y00716; s sequence, including the also found waeble, W.; Dierich, M.; W. 799-802, 1991 Lement factor H: two facto. A60238. MITD:0118202	B42755 G02913 I57998 A42799 I54479 S01896 I53821 JC5138 WMBEZE WMBEZE WMBELE
pression of an a 295 translation translation an alternatively tudies on the co 213 70',35 <sim> serer, A.; Horne</sim>	nko of	short splice form - hu factor H-related protei revision 23-Feb-1996 #t [27877; A61103; A26505; is, T.J.R.; Sim, R.B. id sequence of human co ID:88134059 3; EMBL:Y00716; NID:932 including the amino en Dierich, M.; Weiss, E. 1991 Dor H: two factor H prot	755 759 9913 9913 9918 9918 9918 9918 9918 8918 8
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A;Pathway: complement alternate pathway
C;Superfamily: complement factor H; complement factor H repeat homology
C;Superfamily: complement factor H; complement alternate pathway; glycoprotein; plasma
F;I-18/Domain: signal sequence #status predicted <SIG>
F;19-449/Product: complement factor H, short splice form #status experimental <MAT>
F;21-80/Domain: complement factor H repeat homology <FH01>
F;31-80/Domain: complement factor H repeat homology <FH02>
F;146-205/Domain: complement factor H repeat homology <FH03>
F;210-262/Domain: complement factor H repeat homology <FH04>
F;210-262/Domain: complement factor H repeat homology <FH05>
F;267-320/Domain: complement factor H repeat homology <FH06>
F;367-320/Domain: complement factor H repeat homology <FH06>
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C;Comment: Factor H has also been found bound to cell membranes in an unknown manner. Hc
C;Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver.
C;Genetics: <HF1>
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A;Accession: S10479
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A;Contents: annotation; NMR structure determination, residues 264-292
R;Kristensen, T.; Wetsel, R.A.; Tack, B.F.
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A;Map position: 1932-1932
A;Note: the correspondence bet
C;Function:
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A;Gene: GDB:HF2; HF
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A; Residues: 226-401, '
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                                          RESULT
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Best Local
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                                                                                                                                                 319 RCTLKPCDYPDIKHGGLYHENMRRPYFPV 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the correspondence between the two loci and the sequences indicated is unclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                      RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                     LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
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                                                                                                                                                                                                                                                                                                   LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
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A;Note: 402-Tyr was also found
A;Note: parts of this sequence, including the amino and carboxyl ends of the mature
R;Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
Eur. J. Immunol. 21, 799-802, 1991
A;Title: Human complement factor H: two factor H proteins are derived from alternati
                                                                 R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Biochim. Biophys. Acta 1289, 305-311, 199. A;Title: Factor H co-purifies with thromb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: Partial characterization of human complement factor H by protein and A;Reference number: A61565; MUID:86188123
A;Accession: A61565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M17517; NID:g180497; PIDN:AAA52016.1; PID:g180498
A;Note: parts of this sequence were determined by protein sequencing
R;Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbell, R.D.; Sim, R.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Sequence analysis of a cDNA clone encoding the C-terminal end of human A;Reference number: A54726; MUID:88025472 A;Accession: A54726
                                                                                                                                                                                                                                                                                                                                 A; Reference number: I56100; MUID:91201892
A; Accession: I72654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Contents: annotation; NMR structure determination, residues 264-292
R;Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D.
J. Mol. Biol. 219, 717-725, 1991
A;Title: Three-dimensional structure of a complement control protein module in soluti
A;Reference number: A49224; MUID:91278097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 19-20,'Q',22-29,'V',31-33,'Q',35 <SIM>
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Biochem. J. 205, 285-293, 1982
A;Title: Purification and structural studies on
A;Reference number: A26505; MUID:83048213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Ripoche, J.; Day, A.J.; W. Biosci. Rep. 6, 65-72, 1986
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A; Residues: 'DFRN', 579-1231 <DAY>
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A; Residues: 1-56;1177-1231 <EST>
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A; Residues: 1-1231 <RIP>
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A; Reference number: $66298; MUID: 96205365
A; Accession: $66298
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Cloning of the 1.4-kb mRNA species of human complement factor H reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.; Weiss, J. Immunol. 146, 3190-3196, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Solution structure of the fifth repeat of factor H: A second example of the A; Reference number: A44551; MUID:92232649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A26505
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A; Residues: 'METO
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                                                                                                                                                                            A;Cross-references: GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767
                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1047-1231
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                                                                                                                                                                                                                          1047-1231 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        annotation; NMR structure determination,
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                                                                            fies with thrombospondin isolated from platelet secretate
                                                                                                                  1996
                                                                                                                                                     Tetoz, T.; Areliano, A.; Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the complement-system control protein
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F:1048-1102/Domain: complement factor H repeat homology <FH18>
F:1109-1163/Domain: complement factor H repeat homology <FH19>
F:1167-1228/Domain: complement factor H repeat homology <FH19>
F:1167-1228/Domain: complement factor H repeat homology <FH19>
F:21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F:217-81048-1091,107-1926,931-973,959-984,989-1032,1018-1043,1048-1091,1077-F:217/Binding site: carbohydrate (Asn) (covalent) #status experimental F:718,1029,1095/Binding site: carbohydrate (Asn) (covalent) #status predicted
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F;811-864/Domain:
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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 411-419;574-578,580-582 <CAR>
A;Residues: Factor H has also been found bound to cell membranes in an unknown manner.
C;Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in live
C;Genetics: <HFI>
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                                        241 LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAP 300
                                                                                                                                              199
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                                                                                                                                                                                                                                                                                                                                                          PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                              SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
                                                                                                                                                                                                   SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                            KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 138
EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMYCRKGEWVALNPLR 78
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A;Map position: 1

A;Map position: 1

A;Map position: 1

C;Superfamily: complement factor H; complement factor H repeat homology C;Keywords: complement alternate pathway; duplication; glycoprotein; plic;Keywords: complement factor H status predicted <SIG>
F;1-18/Domain: signal sequence #status predicted <MPT>
F;19-1234/Product: complement factor H #status predicted <MPT>
                   F:1053-1107/Domain: complement factor H repeat homology <FH18>
F:1114-1168/Domain: complement factor H repeat homology <FH19>
F:1172-1233/Domain: complement factor H repeat homology <FH19>
F:1172-1233/Domain: complement factor H repeat homology <FH20>
F:21-66.52-80.85-129.114-141.146-192.178-205.210-251.237-262.267-309.294-320.325-374.
F:21-66.52-80.85-129.114-141.146-192.178-205.210-251.237-262.267-309.294-320.325-374.
F:21-66.52-80.85-129.114-141.146-192.178-205.210-251.237-262.267-309.294-320.325-374.
F:21-66.52-80.85-129.114-141.146-192.178-205.210-251.237-262.267-309.294-320.325-374.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J02891; NID:g193805; PIDN:AAA37795.1; PID:g553926 C;Comment: Two codominant alleles of factor H are present in mice. C;Comment: Factor H functions as a cofactor in the inactivation of C3b by
      F;676,721,773,801,1030,1061,1225/Binding site:
                                                                                                                                                                                                                                     F;936-989/Domain:
                                                                                                                                                                                                                                                                F;867-931/Domain:
                                                                                                                                                                                                                                                                                                                                                         F;629-683/Domain:
F;690-743/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;146-205/Domain:
F;210-262/Domain:
F;246-248/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;19-1234/Product: complement factor H **status predicted < F;21-80/Domain: complement factor H repeat homology <FH01> F;85-141/Domain: complement factor H repeat homology <FH02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: GB:M31979; NID:g193726; PIDN:AAA37762.1; PID:g193729 R;Munoz-Canoves, P.; Tack, B.F.; Vik, D.P. Biochemistry 28, 9891-9897, 1989 Biochemistry 28, 9891-9897, 1989 A;Title: Analysis of complement factor H mRNA expression: Dexamethasone & A;Reference number: I49728; MUID:90148935 A;Accession: I49728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Haraoa, 1.
J. Immunol. 144, 358-362, 1990
A;Title: Demonstration of an unusual allelic variation of mouse factor H by
                                                                                                                                                                                          F;994-1048/Domain: complement factor H repeat homology <FH17>
                                                                                                                                                                                                                                                                                                 F;808-861/Domain:
                                                                                                                                                                                                                                                                                                                               F;752-802/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;509-564/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;448-505/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-19 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-18 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 22-Jun-1999
C;Accession: A26154; I49711; I49728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Cross-references: GB:M12660; NID:g193724; PIDN:AAA37759.1; PID:g387181
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                                                                                                                                                                                                                 complement factor H repeat homology <FH15>
complement factor H repeat homology <FH16>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Soames, C.J.; Day, A.J.; Sim, R.B.
Blochem. J. 315, 523-531, 1996
A;Title: Prediction from sequence comparisons of residues of factor H involved A;Reference number: $65551; MUID:96202005
A;Accession: $65551
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C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C;Accession: S65551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F;355-412/Domain: complement factor H repeat homology <FHR3>
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256 NGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWIPAPRCTLKPCDYPDIKHG 315
                                               123 VILNGQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ICRKKPCGHPGDTPFGSFRLAVGSQFEFGAKVVYTCDDGYQLLGEIDYRECGADGWINDI 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMYCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                       GTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLCEVVKCLPVTELENGRIVSGAAETDQEYYFGQVVRFECNSGFKIEGHKEIHCSENGLW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDCKGPPPRENSEILSGSWSEQLYPEGTQATYKCRPGYRTLGTIVKVCKNGKWVASNPSR 78
                                                                                          DVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP 255
                                                                                                                                                                                                                                 GSPHLAEGNQFEYGAKVVYTCDEGYQMVGEMNFRECDTNGWTNDIPICEVVKCLPVTEPE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCTLKPCDYPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                         NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                                                                                                                                  NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                       154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             al Similarity
216; Conserv
                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67.2%;
65.7%;
                                                                                                                                                                                                                                                                                                                                          48.1%; Score 60.9%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             37; Mismatches
                                                                                                                                                                                                                                                                                                                         33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1261; DB 1; Length 1234; Pred. No. 1e-82;
                                                                                                                                                                                                                                                                                                                                              Score 903; DB 2; Pred. No. 2.3e-57;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76;
                                                                                                                                                                                                                                                                                                                           64;
                                                                                                                                                                                                                                                                                                                                                                 Length 669;
                                                                                                                                                                                                                                                                                                                                                                                                                                         <FHR6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <FHR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              <FHR5>
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C; Keywords: glycoprotein
F; 89-145/Domain: complement factor H repeat homology <FH01>
F; 89-145/Domain: complement factor H repeat homology <FH02>
F; 334-389/Domain: complement factor H repeat homology <FHR1>
F; 450-502/Domain: complement factor H repeat homology <FH03>
F; 569-624/Domain: complement factor H repeat homology <FH03>
F; 682-738/Domain: complement factor H repeat homology <FH06>
F; 935-989/Domain: complement factor H repeat homology <FH05>
F; 935-989/Domain: complement factor H repeat homology <FH06>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        probable complement regulatory plasma protein SB1 - barred sand bass C;Species: Parablax neblifer (barred sand bass)
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 08-Oct-1999
C;Accession: S46199; S77894
C;Accession: S46199; S77894
C;Accession: S46199; S77894
C;Accession: A; Kaidoh, T; Zipfel, P.F.; Gigli, I.
Blochem. J, 301, 391-397, 1994
A;Title: Cloning and characterization of a cDNA representing a putative complement-re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: SB1
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 526-532,'X',534-537;809-817,'X',819-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: liver A; Accession: S77894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-1053 <DAH1>
A;Cross-references: EMBL;L21703; NID:g639894; PIDN:AAA92556.1; PID:g639895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: $46199; MUID: 94318039 A; Accession: $46199
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                                                                                                                                                                                                                                                                                                                   219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316 GLYHENMRRPYFP 328
397 ENIQDAVIVGTDKQIYNLNQKAIY 420
                                                                                                                                                                                                              278
                                                                                                                                                                                                                                                                                                                                                                     200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                 PDIKHG-----GLYHENMRRPY 326
                                                                                                                                                         -PLRI-----KHRTGDEITYQCRNGFYPATRGNT-AKCTSTGWIPAPRCTLKPCDY 309
                                                                                                                                                                                                           GTRYEPAYRNLFSPGETLKVICARTSWISTPQETSVVTTCQDNGEWSIRPTCQEVRCSNR 337
                                                                                                                                                                                                                                                                                                                   GNVPGAIREYKENDVLHYECDRAFKHIDR-PSTCIKQGIKAEWSPTPLCESIKCRLTIMD
                                                                                                                                                                                                                                                                                                                                                                                                                      GG----PEEATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQCPLIHVDNNVQVI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
                                                                                                  RPEHVDSWDVRSWERYTLDDNTRYWCKRG-YKRTGGVTWATCGRNGWMPNPLCEVKTCSK 396
                                                                                                                                                                                                                                                                                                                                                                  GSPISQKITYKENERFQYKCNMGYEYSERGDAVCTESG----WRPLPSCEEKSC-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EASYPGGROVRVGCNVGYS--GFFKLVCVEGKWETRG--AKCOPRSCGHPGDAOFADFHL 102
                                                                                                                                                                                                                                                                  ----DNPYTP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134;
                                                                                                                                                                                                                                                                     -NGDYS-----
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                                                                                                                                                                                                                                                                                                                                                                          249
                                                                                                                                                                                                                                                                     260
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C4BP alpha (C;Species: (C;Date: 10-9) C;Accession R;de Frutos,
                                                                                                                                                                                                                      C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Accession: A33568; S02372; A90326; A24182; A93134; S29492; A31785; I52244; A R:Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. 165, 138-144, 1989 A;Title: Molecular cloning of the cDNA coding for proline-rich protein (PRP):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL: 235490

A:Cross-references: EMBL: 235490

C:Superfamily: C4b-binding protein alpha chain; complement f F:50-107/Domain: complement factor H repeat homology <FH1>
F:112-169/Domain: complement factor H repeat homology <FH3>
F:114-234/Domain: complement factor H repeat homology <FH3>
F:339-294/Domain: complement factor H repeat homology <FH4>
F:299-360/Domain: complement factor H repeat homology <FH5>
F:364-422/Domain: complement factor H repeat homology <FH5>
F:364-480/Domain: complement factor H repeat homology <FH5>
F:426-480/Domain: complement factor H repeat homology <FH7>
F:484-538/Domain: complement factor H repeat homology <FH8>
A;Cross-references: GB:M31452; NID:g190501; PIDN:AAA36507.1; A;Note: the authors translated the codon GGA for residue 492 R;Lintin, S.J.; Lewin, A.R.; Reid, K.B.M. FEBS Lett. 232, 328-332, 1988
                                                                                                                                                                                                                                                                                                                                                                                   C4b-binding protein alpha chain precursor - human N:Alternate names: C4BP; proline-rich protein C:Species: Homo sapiens (man)
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                                                                                                                                                                                A;Reference number: A33568; MUID:90073699 A;Accession: A33568
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A;Accession: $53711
A;Status: preliminary; nucleic acid sequence
A;Molecule type: mRNA
A;Residues: 1-597 <DEF>
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R;de Frutos, P.G.; Dahlbaeck, B.
Biochim. Biophys. Acta 1261, 285-289, 1995
A;Title: cDNA structure of rabbit C4b-binding
                                                                                                                          A; Residues:
                                                                                                                                                A; Molecule type: mRNA
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Best Local
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Date: 10-Sep-1999 #sequence_revision 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       336 YRPVADEPIIVTCQEDLRWSPFAGCEAICCPHPQLDNGAI-TEHSRNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYP-ATRGNTAKC-TSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRP 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAV--C-TESGWRPLPS-CEEKSC-DNPYIPNG-----DYSPLRIKHRTGDEITYQCRNG 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WSDPLPKCEIVKCEPPPNIINGKHNGG----NEDIHTYGSSVTYSCNPRFSLLGEASISC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYKIEGDEEMHC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFCVKKRCRNPGDLPNGQVEVK--TDFSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTD----G 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DCGP-PPHLLFASSISELSENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW---SYD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLG-NVIMVCR-KGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SSLIHCELDSKWNPSPPVCESNSCLGLPNVPHASQQGYQWSTKEGVYSVGTELRYKCRPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TVKNKTVGVWSPSPPVCKEIICSPPNVPHGKIISGFGPIYNYKDSIMYTCIDGFVL--RG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S----DDGFWSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106;
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                                                                                                                 1-597 <MA1>
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30.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 356; DB 1
Pred. No. 3e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           not shown
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as Glu
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                                                                                                                                                                                                                               identity
            A;Cross-references: GB:M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500 t;Comment: C4BP controls the classical pathway of complement activation. It binds as the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement C;Comment: C4BP occurs in plasma in two forms, both of which bind complement fragment isulfide bonds. The beta chain binds the vitamin K-dependent plasma protein S. A mino
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A:Note: this peptide appears to bind protein S
R;Dahlback, B.; Smith, C.A.; Muller-Eberhard, H.J.
Proc. Natl. Acad. Sci. U.S.A. 80, 3461-3465, 1983
A;Title: Visualization of human C4b-binding protein and its complexes with vitamin K-A;Reference number: A93950; MUID:83221615
A;Contents: annotation; electron microscopy; three-dimensional structure; ligand bind R;Aso, T.; Okamura, S.; Matsuguchi, T.; Sakamoto, N.; Sata, T.; Niho, Y.
Blochem. Blophys. Res. Commun. 174, 222-227, 1991
A;Title: Genomic organization of the alpha chain of the human C4b-binding protein gen A;Reference number: 152244; MUID:93113199
A;Attrice of the service of the service of the human C4b-binding protein gen A;Reference number: 152244
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A;Title: The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein A;Reference number: $29492; MUID:93146164
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A;Accession: A24182
A; Molecule type: DNA
A; Residues: 1-597 <ASO>
                                                           A; Status: translation not shown; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 495-505, 'x', 507-510, 'X', 512-515 <SUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 263, 17034-17039, 1988
A;Title: Binding site for vitamin K-dependent protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Suzuki, K.; Nishioka, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 381-404 <HES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 49-81 <CH1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Structure of the gene coding for the alpha polypeptide chain of the human co A; Reference number: A43023; MUID:91217619
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J. Exp. Med. 173, 1073-1082, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: A31785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: A31785; MUID:89034204
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A; Residues: 203-288 <LIN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: 92-Thr and 357-His were
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A;Cross-references: GB:X02865; NID:g29564; PIDN:CAA26617.1; PID:g29565
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A; Residues: 17-81 <LI2>
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A;Introns: 48/1; 110/1; 143/2; 172/1; 236/1; 297/1; 362/1; 482/1; 482/1; 540/3 C;Complex: octamer of seven alpha chains and one beta chain C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C;Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein; F;1-48/Domain: signal sequence #status predicted <STG> F;1-48/Domain: signal sequence #status predicted <STG> F;1-50-108/Domain: complement factor H repeat homology <FHL> F;510-108/Domain: complement factor H repeat homology <FH2> F;113-170/Domain: complement factor H repeat homology <FH2> F;175-234/Domain: complement factor H repeat homology <FH5> F;299-360/Domain: complement factor H repeat homology <FH5> F;399-360/Domain: complement factor H repeat homology <FH5> F;309-360/Domain: complement factor H repeat homology <FH5> F;309-3
A;Cross-references: GB:M36470
A;Experimental source: clone 31-1
R;Kim, Y.U.; Kinoshita, T.; Molina, H.; Hourcade, D.; Seya, T.; Wagner, L.M.; Holers, V. J. Exp. Med. 181, 151-159, 1995
A;Title: Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of bc A;Reference number: 148306; MUID:95105691
A;Accession: I48306
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A; Map position: 1q32-1q32
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A;Accession: A45900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L-PSCEEKSCDN-PYIPNGDYS--PLRIK---HRTGDEITYQCRNGFYPAT-RGNTAKC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVL--RGSSVIHCDADSKWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KPPPDIRNGRHSGE----ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FTLTGGNV----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSTGWIPAPRCTLKPCDYPDIKHGGLYHENMRRP----YF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAV--C-TESGWRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LRNGQVEIKTDLSFGSQIEFSCSEGFFLIGSTTSR-CEVQDRGVGWSHPLPQCEIVKC 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTF--CIYKRCRHPGE----- 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GDB:120568; OMIM:120830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.8%;
29.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 4.8e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 597
                                                                                                                                                                                                                                                                                                                                                                                                                                     IV. Alternative splicing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
                                                                                                                                                                                                                                                                                                                                                                                                                                            of Cr2
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           A; Molecule type: DNA
A; Residues: 1-683,'X',685-894,'A',896-1000,1451-1471,'X',1473-2489 <VIK2>
A; Cross-references: GB:L17418; NID:g306678; PID:g306680
A; Wong, W.W.; Cahill, J.M.; Rosen, M.D.; Kennedy, C.A.; Bonaccio, E.T.; M
J. Exp. Med. 169, 847-863, 1989
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F;399-458/Domain: complement factor H repeat
F;467-523/Domain: complement factor H repeat
F;531-587/Domain: complement factor H repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 21-367 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Gene: Cr2
                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                 A; Accession: I56203
                                                                                                                                                                                                                                                              A;Cross-references: GB:L17418; NID:g306678; PID:g451303
                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 APRCTLKPCD-YPD-IKHGGLY 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 18.8%;
Local Similarity 28.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPTCEVKSCDAIPNHLLHGRVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 353; Db ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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R:Vik, D.P.; Wong, W.W.
J. Immunol. 151, 6214-6224, 1993
A;Title: Structure of the gene for the F allele of complement receptor type 1 and A;Reference number: 156203; MUID:94065175
A;Accession: I73012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U17128; NID:g595980; PIDN:AAA78271.1; PID:g595982 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 24-Nov-1999 #text_change 31-Jan-2000
C;Accession: I73012; I56203; A47602; S03291; S03843; A28507; A24748; B24748;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement C3b/C4b receptor, membrane-bound form precursor - human N;Alternate names: complement C3b/C4b receptor; complement receptor type 1 (CR1); sur N;Contains: complement C3b/C4b receptor, secreted form
                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-683, 'X', 685-1133, 'X', 1135-1471, 'X', 1473-2489 <VIK1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 SDQT-YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SNGDFYSSSRD---SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPP 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HINTG--IEFGSTITYSCNQGYRLIGD-SSATCIVSDNTVMWDNDMPLCESIPCESPPAI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDGWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTG-WI-P 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCSDD----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDKSEFAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PQCIPRVKCPMPEIENGLVESGFKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PKCV-EISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVC-TESGWR-P 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LPTCFMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPG-YTLIGTNLVECTSLGTWSNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              repeat homology <FH02>
H repeat homology <FH03>
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homology <FH08>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             homology <FH04>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 676;
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Bonaccio, E.T.; Morris,
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F:1004-1061/Domain: complement factor F:1066-1132/Domain: complement factor F:1138-1133/Domain: complement factor F:1138-1135/Domain: complement factor F:1197-1253/Domain: complement factor F:1258-1316/Domain: complement factor F:1258-1316/Domain: complement factor
                                                                                                                                                                                                                                                                                                                                                                                                                                        F;688-743/Domain: complement F;747-803/Domain: complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-2489/Product: complement C3b/C4b receptor, membrane-bound form #status predicted F;42-384/Product: complement C3b/C4b receptor, secreted form #status predicted <MATS>
F;43-99/Domain: complement factor H repeat homology <FRONDAMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GDB:119800; OMIM:120620
A;Map position: 1932-1932
A;Introns: 41/1; 101/1; 134/2; 163/1; 296/1; 355/1; 389/2; 418/1; 491/1; 551/1; 584/2; 1484/2; 1513/1; 1646/1; 1705/1; 1739/2; 1768/1; 1844/1; 1904/1; 1937/2; 1966/1; 2099, C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C;Keywords: duplication; 91ycoprotein; transmembrane protein
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A;Residues: 953-1221,'FV,,1224-2064,'I',2066-2276,'P',2278-2299,'H',2301-2325,'T',2327-A;Cross-references: GB:X05309; NID:g30196; PIDN:CAA28933.1; PID:g809019
R;Wong, W.W.; Klickstein, L.B.; Smith, J.A.; Weis, J.H.; Fearon, D.T.
Proc. Natl. Acad. Sci. U.S.A. 82, 7711-7715, 1985
A;Title: Identification of a martial cDNA clone for the human receptor for complement in the complement in 
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F;358-416/Domain: complement
F;421-487/Domain: complement
F:423-549/Domain: complement
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F;166-232/Domain:
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A:Residues: 26-584 <HOU>
A:Cross references: EMBL:X14362; NID:g30197; PID:g736240
A:Cross references: EMBL:X14362; NID:g30197; PID:g736240
A:Experimental source: clone CR1-4
R:Klickstein, L.B.; Bartow, T.J.; Miletic, V.; Rabson, L.D.; Smith, J.A.; Fearon, D.T.
J. Exp. Med. 168, 1699-1717, 198
A:Title: Identification of distinct C3b and C4b recognition sites in the human C3b/C4b
A:Reference number: S03843; MUID:89035992
F;1321-1387/Domain: complement
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A;Accession: A28507
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R;Klickstein, L.B.; Wong, W.W.; Smith, J.A.; Weis, J.H.; Wilson, J.G.; Fearon, D.T.
J. Exp. Med. 165, 1095-1112, 1987
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A; Residues: 311-333,729-745;831-845 <WO2>
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A;Accession: A47602
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. 168, 1255-1
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1255-1270, 1988
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F;1969-2035/Domain:
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F;1846-1902/Domain:
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F;1647-1703/Domain:
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F;1454-1511/Domain:
F;1516-1582/Domain:
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                        270 DEITYQCRNGFYPATRGNTAKCTSTG-WIP-APRCTLKPCD 308
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QEVFYSCEPG-YDLRGAASMRCTPQGDWSPAAPTCEVKSCD 359
                                                                                                   EPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSLNEVVEFRCQPG
                                                                                                                          DEEMHC--SDD--GFWSKEKPKC-VEISCKSPDVINGSPIS-QKIIYKENERFQYKCNMG
                                                                                                                                                                                                      -RCRRKSCRNPPDPVNGMVHVIKG--IQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 153
                                                  FVMKGPRRVKCQALNKWEPELPSC-SRVCQPP--PDVLHAERTQRDKDNFSP--
                                                                          YEYSERGDAVCTE-SGWRP-LPSCEEKSCDNPYIPN------GDYSPLRIKHRTG
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F;141-207/Domain: complement factor H repeat homology <FH03>
F;213-268/Domain: complement factor H repeat homology <FH04>
F;272-328/Domain: complement factor H repeat homology <FH06>
F;333-391/Domain: complement factor H repeat homology <FH06>
F;396-462/Domain: complement factor H repeat homology <FH06>
F;396-462/Domain: complement factor H repeat homology <FH09>
F;470-526/Domain: complement factor H repeat homology <FH09>
F;722-78/Domain: complement factor H repeat homology <FH10>
F;1041-1107/Domain: complement factor H repeat homology <FH11>
F;1172-1228/Domain: complement factor H repeat homology <FH11>
F;1233-1291/Domain: complement factor H repeat homology <FH12>
F;1432-1489/Domain: complement factor H repeat homology <FH15>
F;1432-1481/Domain: complement factor H repeat homology <FH15>
F;1625-1681/Domain: complement factor H repeat homology <FH15>
F;1823-879/Domain: complement factor H repeat homology <FH15>
F;1823-1879/Domain: complement factor H repeat homology <FH15>
F;1823-1879/Domain: complement factor H repeat homology <FH15>
F;1824-1940/Domain: complement factor H repeat homology <FH15>
F;1824-1940/Domain: complement factor H repeat homology <FH18>
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                                                                                                               A;Reference number: S03291; MUID:89010527
A;Accession: S03292
A;Status: nucleic acid sequence not shown:
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Duplication and divergence of the amino-terminal coding region of the complement A;Reference number: A34924; MUID:90110163
A;Accession: A34924
A;Molecule type: DNA
A;Residues: 1-479 < NUID: A34924
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A;Molecule type: DNA
A;Residues: 'FPFFAFR',452-482 <HO2>
A;Cross-references: EMBL:X14360
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1988
                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:J05195
R;Hourcade, D.; Miesner, D.R.; Atkinson, J.P.; Holers, V.M.
J. Exp. Med. 168, 1255-1270, 1988
                                                                                                                                                                                                                                                                                                                     A; Title: Identification of an alternative polyadenylation site in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                            Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1557 PPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIVRFRCQPGFVMVGSHTVQCQTNGRWGP 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1500 ISNGDFYSNNR---ASFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDDQVGVWSSP 1556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 PENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCS--DD--GFWSKE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     296 -WIP-APRCTLKPCD--YPDIKHGGLYHENMRRPYFPV 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 -LPSCEEKSCDNPYIPNGDYSPLRIKHR----TGDEITYQCRNGFYPATRGNTAKCTSTG 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG----WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 SDQTYPEGTQAIYKCRPGYRSLGNVIMV-CRKG-EWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DWSPEAPRCTVKSCDDFLGQLPHG-----RVLFPL 1702
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                                                                                                                                                                                                                                                                                                                                     the human C3b/C4b rec
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73 LQLKCGPPPEIPFAVHDGSSFSGEYDLDAEGLSISKCLLNRKNVAQWFGPDLRCKARACP 132

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C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology F;43-99/Domain: complement factor H repeat homology cFH01> F;104-161/Domain: complement factor H repeat homology cFH02> F;166-232/Domain: complement factor H repeat homology cFH03> F;238-293/Domain: complement factor H repeat homology cFH04> F;238-293/Domain: complement factor H repeat homology cFH05> F;388-293/Domain: complement factor H repeat homology cFH06> F;388-293/Domain: complement factor H repeat homology cFH06> F;388-416/Domain: complement factor H repeat homology cFH06> F;328-416/Domain: complement factor H repeat homology cFH07>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein T07H6.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         망
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A;Introns: 14/1; 75/1; 102/3; 128/1; 186/1; 272/2; 326/1; 361/1; 422/1; 475/1; 527/1 C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: Z18586
A; Accession: T16833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U53344; NID:g1255886; PID:g1255889; PIDN:AAA96225.1; GSPDB:G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, April 1996 A;Description: The sequence of C. elegans cosmid T07H6
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                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-560 <GEI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                        Local Similarity
                                                              17 CHPLPNIENGFIRTA--GDLRF--GSNAEYGCNKGYILVGASQRRCQANKEWSSSQPVCR 72
         60 -----
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                                                                                                                            3 CNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKG-EWVALNPL-- 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTGDEITYQCRNGFYPATRGNT-AKCTSTG-WIP-APRCTLKPCD 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --WINDIPICEVVKC-LPVTAPENGKIVSSAMEPDREY-HFGQAVRFVCNSG-----YK 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GQEVFYSCEPGY--DLRGSTYLHCTPQGDWSPAAPRCEVKSCD 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QPGFHMKGPSHVKCQALNKWEPELPSC-SRVCQPP--PDVLHAERTQRDKDNFSP----
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                                                                                                                                                                                                                        18.0%; Score 337.5; DB 2 23.0%; Pred. No. 5.8e-17;
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                                                                                                                                                                                             57; Mismatches 142;
                                                                                                                                                                                                                                                            DB 2; Length 560;
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         -----RKCQKRPCG 68
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C;Superfamily: herpesvirus complement control protein; complement factor H repeat homol
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A;Molecule type: DNA
A;Residues: 1-360 <ALB>
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Best Local
291 CNQNCTTS 298
                                   287 NTAKCTST 294
                                                                                                                                       189 KQCSETGRWVPDEETKCEFKVCKIPQVANGHVEVRKT--SNNVQYQYVNIKCDKGFRLQG
                                                                                                                                                                             172 MHCSDDGFW-SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQY---KCNMGYEYSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 LKPCDYPDIKHGGL 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   363 CHNWPPRVPHARI--LFSKSSHGSIAKYECNNGYHPNRNNQIIKCLYGEWTKDGPPMKCL 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      243 EEIRCSVLPTLPNGYIEGSETSFGAVAVFRCLETMTHEGASKAKCMEDGQWSAPIPRCLA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 VEISCK-SPDVING------SpI----
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                                                                                                                                                                                                                                                                                                                                        60
                                                                                                                                                                                                                                                                                                                                                                    24 PKRNRYVSLRYVNITN--SSGSYPNGTTLQVTCRKGY--IGRQIQTVTCVNGNWTVPN-- 77
                                                                                                                                                                                                                                                                                                                                                                                                                    ω
                                                               ETPNMCKNGVWFPALPTCEK-----PAPPRGD-----MPHIDSGEDTST------PSGRN 290
                                                                                                 RGDAVCTESGWRP-LPSCEEKSCDNPYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRG 286
                                                                                                                                                                                                                NWTPRPPICEITKCKPPPTIANGTHTNI-----KEYYTYLDAVTYSCNDETKLTLTGPSS 188
                                                                                                                                                                                                                                                    -WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYK--IEGDEE 171
                                                                                                                                                                                                                                                                                                                            RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC--DTDG-- 115
                                                                                                                                                                                                                                                                                                                                                                                                        PRRNTEI-----LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI--MVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDN--PYIPNGDYSPLRIKHRTGDEITYQCRNGFYPATRGNTAKCTSTGWI---PAPRCT 303
                                                                                                                                                                                                                                                                                          -ECQKRRCSTPADLLNGWYTVT-GNLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PSWCEHPSKTYGTL 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQKIIYKENERFQYK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                       103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SCRVPHIQNGKIRDKSEGQLIASGSKVIVECNKQHEANIDERLICSNSTWSHVPVCSPLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CSRPSSPLHGKVVGSSLT-----YQSVVTYSCDHGYRLVGQVQRICLAEGIWGGNEPRC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDG-WTNDIPICEVVK 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               17.9%; Score 335; DB 2; 33.4%; Pred. No. 5.5e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -CNMGYEYSERGDAVCTESGWRPLPSCEEKS 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 360;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
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R;Hillarp, A.; Thern, A.; Dahlback, B.
J. Immunol. 153, 4190-4199, 1994
A;Title: Bovine Cdb binding protein. M
A;Reference number: I46001; MUID:95015
                                                                                                                                                  C:Species: Bos primigenius taurus (cattle)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I46001; S43190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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F:38-94/Domain: complement factor H repeat homology <FH1>
F:99-156/Domain: complement factor H repeat homology <FH2>
F:161-227/Domain: complement factor H repeat homology <FH3>
F:233-288/Domain: complement factor H repeat homology <FH4>
F:233-288/Domain: complement factor H repeat homology <FH4>
F:234-352/Domain: complement factor H repeat homology <FH5>
F:357-413/Domain: complement factor H repeat homology <FH5>
F:357-413/Domain: complement factor H repeat homology <FH6>
F:341-444/Domain: transmembrane #status predicted <TMM>
F:421-444/Domain: transmembrane #status predicted <TMM>
F:421-331,346,450,482,483/Binding site: carbohydrate (Asn) (covalent) #status predict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Residues: 39-51 <SA2>
C; Comment: This protein plays a critical role in protection against complement mediat C; Comment: This protein plays a critical role in protection against complement mediat C; Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C; Keywords: 91ycoprotein, transmembrane protein C; Keywords: 91ycoprotein, transmembrane protein SIG>
F; 1-36/Domain: signal sequence #status predicted <SIG>
A; Accession: I46001
                                                                                                                                                                                                                                                                             C4b-binding protein alpha chain - bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-497 <SAK>
A; Accession: PC2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Sakurada, C.; Seno, H.; Dohi, N.; Takizawa, H.; Nonaka, M.; Okada, N.; Okada, H. Biochem. Biophys. Res. Commun. 198, 819-826, 1994
A;Title: Molecular cloning of the rat complement regulatory protein, 512 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement regulatory protein, 512 antigen precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 21-Jan-2000 C;Accession: JC2054; PC2027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: JC2054; MUID: 94161746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 ---W-IPAPRCTLKPCDYPDIKHGGLYHENMRRPYF 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     113 --NTDIRFGSSITYTCNEGYRLIGSSSAMCIISDQSVAWDAEAPICESIPCEIPPSIP-N 169
                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESIWNSSVPVCEQVICKLPQDMSGFQKGLQMKKDYY 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSCFKVKSCGAFLGELPNGHVFVPQNL--QLGAKVTFVCNTGY--QLKGNSSSHCVLDGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QCIELNKCTPPHVENAVIVSKNKSLFSLRDMVEFRCQDGFMMKGDSSVYCRSLNRWEPQL 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCVEIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GDFFS----PNREDFHYGMVVTYQCNTDARGKKLFNLVGEPSIHCTSIDGQVGVWSGPPP 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GKIVSSAMEPDRE-YHFGQAVRFVCNSG-----YKIEGDEEMHCS----DDGFWSKEKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTD---GWTNDIPICEVVKC-LPVTAPEN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSC-EEKSCDN--PYIPNGD-YSPLRIKHRTGDEITYQCRNGFYPATRGNTAK-CTSTG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ESTFPVGTSLKYECRPGYIKRQFSITCEVNSVWT--SPQDVCIRKQCETPLDPQNGIVHV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JC2054
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.2%; Score 323; DB 2; 28.3%; Pred. No. 5.6e-16;
                          protein. Molecular cloning of the alpha- and beta-chains \mbox{\sc MUID:}95015909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55; Mismatches 144; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 497;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-610 <HIL>
A;Residues: 1-610 <HIL>
A;Residues: 1-610 <HIL>
A;Residues: 1-610 <HIL>
A;Cross-references: EMBL.Z31693; NID:9469117; PIDN:CAA83498.1; PID:9469118
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology <FH1>
F;50-107/Domain: complement factor H repeat homology <FH2>
F;112-169/Domain: complement factor H repeat homology <FH4>
F;239-294/Domain: complement factor H repeat homology <FH4>
F;299-362/Domain: complement factor H repeat homology <FH6>
F;366-425/Domain: complement factor H repeat homology <FH8>
F;487-541/Domain: complement factor H repeat homology <FH8>
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Search completed: November 21, 2000, 16:47:40 Job time: 369 sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116 WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCS 175
                                                                                                                                                  330 LSYKCHFGYKPETDGPTTVTCQSNLEWSPYIECKEVCCPEPNLNNYGSITLH----RRP 384
                                                                                                                                                                                                                272 ITYOCRNGFYPATRG-NTAKCTST-GWIPAPRCTLKPCDYPDIKHGG--LYHENMRRP 325
                                                                                                                                                                                                                                                                                     274 -- EGDSLIHCEADNSWNPPPPTCELNGCLGLPHIPHALWE--RYDHQTQTEQQVYDIGFV 329
                                                                                                                                                                                                                                                                                                                                                                                                              219 VENKTIGVWSPSPPSCKKVICVQPVVKDG-----KITSGFGPIYTYQQSIVYACNKGFRL 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 WSDPLPQCIIAKCEPPPTISNGR--HNGGDED-FYTYGSSVTYSCDRDFSMLGKASISCR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109 KKRCENPGE-----LLNGQVIVKTDYSFGSEIEFSCSEGYVLIGSANSYCQLQDKGVV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 IPPYLDFAFPINELNETRFETGTTLRYTCRPGYRISSRKNFLICDGTDNW----KYKEFCV 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 LPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQ 63
                                                                                                                                                                                                                                                                                                                                                SERGDAV--C-TESGWR-PLPSCEEKSC-DNPYIPNGDYSPLRIKHRTGDE----- 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DD----GFWSKEKPKCVEISCKSPDVINGSPISQKI-----IYKENERFQYKCNMGYEY 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 610;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                 Database :
                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                             Post-processing: Minimum Match 0%
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Gapop 10.0 , Gapext 0.5
                                                                                                   Maximum Match 100%
Listing first 45 summaries
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1497
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Copyright (c) 1993 - 2000 Comp
pir1:*
pir2:*
pir3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir4:*

SUMMARIES

29	28	27	26	25	24	2 3	22	21	20	19	18	17	16	15	14	13	12	11	10	9	8	7	0	ر ن	4	ω	2		No.	Result	
270.5	270.5	270.5	272	273.5	274	274	274.5	4	N	276.5	7		284.5	284.5	284.5	289.5	290.5	298.5	301	301.5	302	303	332.5	4	699	1024	4	9	Score		
18.1	18.1	18.1	•	٠		18.3						•	•	٠	•	•	•	•	•	20.1	•		•	29.4	46.7	•	100.0		Match	Query	æ
440	369	362	610	433	384	377	369	349	469	558	560	263	482	263	263	497	2014	2489	676	263	597	597	360	1053	669	1234	1231	449	Length		
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A43519	JC5138	JC5194	A35046	A30550	S01896	I54479	157998	G02913	NBMSC4	S57953	T16833	B72152	A34924	T28450	C36838	JC2054	I36936	173012	A45900	WMVZSP	S53711	NBHUC4	T42921	S46199	S65551	NBMSH	NBHUH	NBHUHS			
=		membrane cofactor		=			ofa	m CD46 -	binding p		ō	B18L protein - var	ω	Ω				C3b/		tein H	C4BP alpha chain p	C4b-binding protei	nt contro	е СО			ь.	complement factor	iption		

4	44	43	42	41	40	39	38	37	36	S	34	ω ω	32	31	30
252	252.5	253	254	255	256.5	257	257.5	260	260.5	262	262	264.5	264.5	265.5	266
16.8	16.9	16.9	17.0	17.0	17.1	17.2	17.2	17.4	17.4	17.5	17.5	17.7	17.7	17.7	17.8
340	1091	345	768	452	618	579	1025	612	768	440	381	360	302	610	482
N	μ	ب	2	Ν	N	N	L	N	N	N	-	1	Н	_	Ν
156234	PL0009	NBMS	I53821	A35068	B42755	A56740	A43526	S23174	A42755	A26359	в26359	WMBE2E	WMBE1E	146001	JC5092
decay-accelerating	complement C3d/Eps	apolipoprotein H p	P-selectin - rat	complement factor	E-selectin precurs	sperm-egg recognit	complement C3d/Eps	endothelial leukoc	P-selectin precurs	decay-accelerating	decay-accelerating	membrane-bound com	secretory compleme	C4b-binding protei	E-selectin - pig

ALIGNMENTS

NBHUHS Complement factor H precursor, short splice form - human complement factor H precursor, short splice form - human complement factor H-related protein; complement protein H C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence_revision 23-Feb-1996 #text_change 22-Jun-1999 C;Accession: S03013; B60238; A27877; A61103; A26505; S10479 C;Accession: J.; Dav. A.J.; Harris, T.J.R.; Sim. R.R.

A;Title: The complete amino acid sequence of human complement factor H. A;Reference number: S00254; MUID:88134059
A;Accession: S03013 A; Molecule type: mRNA A; Residues: 1-449 < RIP>

A; Note: part of this sequence, A; Note: 402-Tyr was also found A;Cross-references: EMBL:X07523; EMBL:Y00716; NID:g32492; PIDN:CAA30403.1; PID:g75807 A;Note: part of this sequence, including the amino end of the mature protein was conf

R;Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H. Eur. J. Immunol. 21, 799-802, 1991
A;Title: Human complement factor H: two factor H proteins A; Reference number: A60238; MUID: 91184292 A;Status: not compared with conceptual translation A; Accession: B60238 are derived from alternativ

A;Molecule type: mRNA A;Residues: 1-33,434-449 <EST> A;Residues: 1-33,434-449 <EST> A;Residues: 1-35,434-449 <EST> A;Residues: 1-35,434-449 <EST> A;Rote: only portions of this 1.8 kilobase mRNA were sequenced R;Schulz, T.F.; Schwaeble, W.; Stanley, K.K.; Weiss, E.; Dierich, M.P. Eur. J. Immunol. 16, 1351-1355, 1986 A;Title: Human complement factor H: isolation of cDNA clones and partial cDNA sequenc A;Reference number: A27877; MUID:87054207 A;Accession: A27877

A;Molecule type: mRNA
A;Residues: 'IL',55-401,'Y',403-449 <SCH>
A;Residues: 'IL',55-401,'Y',403-449 <SCH>
A;Residues: 'IL',55-401,'Y',403-449 <SCH
A;Rote: an additional nucleotide present within the codon for Glu-310 was thought to A;Note: an additional nucleotide present within the codon for Glu-310 was thought to R;Schwaeble, W; Zwirner, J; Schulz, T.F.; Linke, R.P.; Dierich, M.P.; Weiss, E.H.
Eur. J. Immunol. 17, 1485-1489, 1987
Eur. J. Immunol. 17, 1485-1489, 1987
A;Title: Human complement factor H: expression of an additional truncated gene produce A;Reference number: A61103; MUID:88055295

A; Status: not compared with conceptual translation

A; Accession: A61103

A; Molecule type: mRNA A; Residues: 27-76 <SC2>

A;Note: this is a partial sequence of an alternatively spliced 1.8 kilobase mRNA that R;Sim, R.B.; Discipio, R.G. Biochem. J. 205, 285-293, 1982 Biochem. J. 205, 285-293, 1982 A;Title: Purification and structural studies on the complement-system control protein A;Reference number: A26505; MUID:83048213

A;Molecule type: protein
A;Residues: 19-20,'Q',22-29,'V',31-33,'Q',35 <SIM>
R;Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.; Pearce,
Biochemistry 31, 3626-3634, 1992 J.; Driscoll,

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A;Gene: GDB:HF1; HF
A;Cross-references: G
A;Map position: 1q32-C;Genetics: <HF2>
A;Gene: GDB:HF2; HF
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A; Map positi
A; Note: the
C; Function:
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F:325-385/Domain: complement factor H repeat homology <FH06>
F:325-385/Domain: complement factor H repeat homology <FH06>
F:389-442/Domain: complement factor H repeat homology <FH07>
F:21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
F:217/Binding site: carbohydrate (Asn) (covalent) #status shows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Pathway: complement alternate pathway
C; Superfamily: complement factor H; complement factor H repeat homology
C; Superfamily: complement factor H; complement alternate pathway; glycoprotein; plasme
E; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-449/Product: complement factor H, short splice form #status experimental <MAT>
F; 21-80/Domain: complement factor H repeat homology <FH02>
F; 85-141/Domain: complement factor H repeat homology <FH02>
F; 10-262/Domain: complement factor H repeat homology <FH04>
F; 246-248/Region: cell attachment (R-G-D) motif
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A;Recession: S10479
A;Recession: S10479
A;Molecule type: mRNA
A;Residues: 226-401,'Y',403-449 <KRI>
A;Cross-references: GB:M12383; NID:9180472; PIDN:AAA52013.1; PID:9180473
A;Cross-references: GB:M12383; NID:9180472; PIDN:AAA52013.1; PID:9180473
C;Comment: Factor H has also been found bound to cell membranes in an unknown manner. Hc
C;Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver.
C;Genetics: <HF1>
C;Genetics: <HF
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 22-Jun-1999
C;Accession: S00254; A60238; A54726; A61565; A26505; I72654; S66298
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A;Contents: annotation; NMR structure determination, residues 264-292
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                                                                                                                                             complement factor H precursor, long splice form - human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
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Pred. No. 2.5e-106;
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A; Molecule type: mrNA
A; Molecule type: mrNA
A; Residues: 'DFRN', 579-1231 <DAY>
A; Residues: 'DFRN', 579-1231 <DAY>
A; Cross-references: GB: m17517; NID: g180497; PIDN: AAA52016.1; PID: g180498
A; Note: parts of this sequence were determined by protein sequencing
R; Ripoche, J.; Day, A.J.; Willis, A.C.; Belt, K.T.; Campbell, R.D.; Sim, R.B.
Biosci. Rep. 6, 65-72, 1986
Biosci. Rep. 6, 65-72, 1986
A; Title: Partial characterization of human complement factor H by protein and
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A;Title: Sequence analysis of a cDNA clone encoding the C-terminal end of human compl
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A;Title: Purification and structural studies on the complement-system control protein
A;Reference number: A26505; MUID:83048213
A;Accession: A26505
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A;Note: parts of this sequence, including the amino and carboxyl ends of the mature p
R;Estaller, C.; Schwaeble, W.; Dierich, M.; Weiss, E.H.
Eur. J. Immunol. 21, 799-802, 1991
A;Molecule type: protein
A;Residues: 411-419;574-578,580-582 <CAR>
C;Comment: Factor H has also been found bound to cell membranes
                                                                                                                                                                                                              A;Cross-references: GB:M65294; NID:g183766; PIDN:AAA35948.1; PID:g183767 R;Carron, J.A.; Bates, R.C.; Smith, A.I.; Tetoz, T.; Arellano, A.; Gordon Biochim. Biophys. Acta 1289, 305-311, 195-311. 195 A;Title: Factor H co-purifies with thrombospondin isolated from platelet A;Reference number: S66298; MUID:96205365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Contents: annotation; NMR structure determination, residues 264-292 R;Norman, D.G.; Barlow, P.N.; Baron, M.; Day, A.J.; Sim, R.B.; Campbell, I.D J. Mol. Biol. 219, 717-725, 1991 A;Title: Three-dimensional structure of a complement control protein module A;Reference number: A49224; MUID:91278097
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A; Residues: 19-20,'Q',22-29,'V',31-33,'Q',35 <SIM>
A; Residues: 19-20,'Q',22-29,'V',31-33,'Q',35 <SIM>
B; Barlow, P.N.; Norman, D.G.; Steinkasserer, A.; Horne, T.J.; Pearce, J.; Driscoll, P.
Biochemistry 31, 3626-3634, 1992
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A; Residues: 'METGRNHLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-56;1177-1231 <EST>
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                                                                                                                                  A; Status: preliminary
                                                                                                                                                                                   A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1047-1231 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: I56100; MUID: 91201892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Cloning of the 1.4-kb mRNA species of human complement factor H reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation; NMR structure determination, residues R; Estaller, C.; Koistinen, V.; Schwaeble, W.; Dierich, M.P.; J. Immunol. 146, 3190-3196, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A44551; MUID: 92232649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Solution structure of the fifth repeat of factor H: A second example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Sim, R.B.; DiScipio,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A61565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A61565; MUID:86188123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translated from GB/EMBL/DDBJ
                                                                                                                                                                                   S66298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METGRNHLNAKI', 1050-1057, 'T', 1059-1102 <RI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.G.
                                                                                                                                                                                                                                                                isolated from platelet secretate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Weiss,
                                                                                                                                                                                                                                                                                                                                                              A.; Gordon,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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in an unknown manner

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F;267-320/Domain: complement factor H repeat homology <FH05>
F;325-385/Domain: complement factor H repeat homology <FH06>
F;389-442/Domain: complement factor H repeat homology <FH06>
F;488-505/Domain: complement factor H repeat homology <FH07>
F;488-505/Domain: complement factor H repeat homology <FH09>
F;509-564/Domain: complement factor H repeat homology <FH10>
F;569-623/Domain: complement factor H repeat homology <FH11>
F;691-744/Domain: complement factor H repeat homology <FH12>
F;753-803/Domain: complement factor H repeat homology <FH13>
F;811-864/Domain: complement factor H repeat homology <FH13>
F;870-926/Domain: complement factor H repeat homology <FH14>
F;871-984/Domain: complement factor H repeat homology <FH16>
F;981-984/Domain: complement factor H repeat homology <FH16>
F;989-1043/Domain: complement factor H repeat homology <FH17>
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F: 146-205/Domain: c
F: 210-262/Domain: c
F: 246-248/Region: c
F: 267-320/Domain: c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1048-1102/Domain: complement factor H repeat homology <FH18>
F;1109-1163/Domain: complement factor H repeat homology <FH19>
F;1109-1163/Domain: complement factor H repeat homology <FH20>
F;1167-1228/Domain: complement factor H repeat homology <FH20>
F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,357
1-803,811-853,839-864,870-915,901-926,931-973,959-984,989-1032,1018-1043,1048-1091,1077-
F;217/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;529,802,822,882,91/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Pathway: complement alternate pathway C;Superfamily: complement factor H; comp C;Keywords: alternative splicing; complete;1:18/Domain: signal sequence #status;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GDB:129095
A;Map position: 1q32-1q32
A;Note: the correspondence bet
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Comment: Alternat
C;Genetics: <HF1>
A;Gene: GDB:HF1; HF
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C; Genetics: <HF2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Comment: Alternative transcipts of 4.3, 1.8, and 1.4 kilobases are expressed in liver
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139
                                                                                                                                                    259
                                                                                                                                                                                                                   241 LPSCEEKSCDNPYIPNGDYSPLRIK 265
                                                                                                                                                                                                                                                                                                                                              181 SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the correspondence between the two loci and the sequences indicated is unclear;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PICEVVKCLPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFW 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SKEKPKCVEISCKSPDVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRP
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complement factor H repeat homology <FH04>
cell attachment (R-G-D) motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                   Matches
1 EDCNELPPRRNTEILTGSWSDQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLR 60
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F;1053-1107/Domain: complement factor H repeat homology <FH18>
F;1114-1168/Domain: complement factor H repeat homology <FH19>
F;11172-1233/Domain: complement factor H repeat homology <FH19>
F;1172-1233/Domain: complement factor H repeat homology <FH20>
F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,F;21-66,52-80,85-129,114-141,146-192,178-205,210-251,237-262,267-309,294-320,325-374,0-802,808-850,836-861,867-920,906-931,936-978,964-989,994-1037,1023-1048,1053-1096,10
F;676,721,773,801,1030,1061,1225/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                 F;752-802/Domain: complement factor H repeat homology <FH13>F;808-861/Domain: complement factor H repeat homology <FH14>F;808-861/Domain: complement factor H repeat homology <FH15>F;936-931/Domain: complement factor H repeat homology <FH15>F;936-989/Domain: complement factor H repeat homology <FH17>F;994-1048/Domain: complement factor H
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F; 325-385/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:M12660; NID:g193724; PIDN:AAA37759.1; R;Natsuume-Sakai, S.; Nonaka, M.; Nonaka, M.; Harada, Y. J. Immunol. 144, 358-362, 1990
A;Title: Demonstration of an unusual allelic variation of mou A;Reference number: I49711; MUID:90111033
A;Accession: I49711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Kristensen, T.; Tack, B.F.
Proc. Natl. Acad. Sci. U.S.A. 83, 3963-3967, 1986
A;Title: Murine protein H is comprised of 20 repeating A;Reference number: A26154; MUID:86233353
A;Accession: A26154
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C:Date: 30-Sep-1987 #text_change 22-Jun-1999
C:Accession: A26154; I49711; I49728
C:Accession: A26154; I49711; I49728
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F; 752-802/Domain:
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F;569-622/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Keywords: complement alternate pathway; duplication;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: complement factor H; complement factor H repeat homology
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A; Residues: 1-19 < RE2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;629-683/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;1-18/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: I49728; MUID:90148935
A; Accession: I49728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-18 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement factor H precursor - mou. N; Alternate names: protein beta-1-H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
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factor H repeat homology <FH07>
factor H repeat homology <FH07>
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Similarity

68.48; 67.08;

Conservative

30;

Score 1024; DB 1; Pred. No. 5.4e-70; D; Mismatches 57;

Indels

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probable complement regulatory plasma protein SB1 - barred sand C;Species: Parablax neblifer (barred sand bass)
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change C;Accession: 346199; 877894
R;Dahmen, A.; Kaidoh, T.; Zipfel, P.F.; Gigli, I.
Blochem. J. 301, 391-397, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Rosidues: 1-669 <500-4
A; Cross-references: GB:X98697; NID:gl419423; PIDN:CAA67257.1; PID:gl419424
A; Cross-references: GB:X98697; NID:gl419423; PIDN:CAA67257.1; PID:gl419424
C; Superfamily: complement factor H; complement homology <FHR1>
F; 255-114/Domain: complement factor H repeat homology <FHR2>
F; 355-412/Domain: complement factor H repeat homology <FHR3>
F; 416-471/Domain: complement factor H repeat homology <FHR8>
F; 416-530/Domain: complement factor H repeat homology <FHR8>
F; 438-592/Domain: complement factor H repeat homology <FHR8>
F; 599-651/Domain: complement factor H repeat homology <FHR8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Bos primigenius taurus (cattle)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change
C;Accession: S65551
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A; Accession: S65551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Prediction from sequence comparisons
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                                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                                                                256 NGDYSP 261
                                                                                                                                                                                                                                                                                                                                                              123 VILNGQAVLPKATYKQNERVQYRCAAGFEYGQRGDTVCTKSGWTPAPTCIEITCDPPRIP 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 LPSCEEKSCDNPYIPNGDYSPLRI 264
                                                                                                                                                                                                                                                                                                                                                                                                              196 DVINGSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESGWRPLPSCEEKSCDNPYIP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 NGKIFSDALEPDQEYTYGQVVQFECNSGYMLDGPKQIHCSAGGVWSAETPKCVEIFCKPP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 GTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPE 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                   NGVYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCKSP 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SNEKPRCVEILCTPPRVENGDGINVKPVYKENERYHYKCKHGYVPKERGDAVCTGSGWSS 258
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                                                                                        #text_change 08-Oct-1999
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C;Keywords: glycoprotein
F;89-145/Domain: complement factor H repeat homology <FH01>
F;89-145/Domain: complement factor H repeat homology <FH02>
F;334-389/Domain: complement factor H repeat homology <FHR1>
F;450-502/Domain: complement factor H repeat homology <FH03>
F;569-624/Domain: complement factor H repeat homology <FH04>
F;782-738/Domain: complement factor H repeat homology <FFH04>
F;743-802/Domain: complement factor H repeat homology <FH05>
F;935-989/Domain: complement factor H repeat homology <FH05>
F;993-1052/Domain: complement factor H repeat homology <FH05>
                                                                                                                                                                                                                                                                                                                                                                   complement control protein homolog ccph - ateline herpesvirus 3 (strain 73)
C;Species: ateline herpesvirus 3
A;Varriety: strain 73
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: SB1
C; Superfamily:
A; Experimental source: strain 73 C; Superfamily: herpesvirus complement control protein;
                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, August 1998 A; Description: Primary structure of the herpesv
                                                                                                                                                                                                                                                                                                            C; Accession: T4292
R; Albrecht, J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics
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A; Residues: 526-532,'X',534-537;809-817,'X',819-826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1053 < DAH1>
A; Cross-references: EMBL:L21703; NID:g639894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning and characterization of a cDNA representing a putative complement-re A;Reference number: S46199; MUID:94318039 A;Accession: S46199
                                                                                             A; Molecule type: DNA
A; Residues: 1-360 < ALB>
                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                        A; Reference number: Z22274
A; Accession: T42921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T42921
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                                                                A;Cross-references: EMBL:AF083424; PIDN:AAC95530.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 NGDYSP 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTRYEP 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNVPGAIREYKENDVLHYECDRAFKHIDR-PSTCIKQGIKAEWSPTPLCESIKCRLTIMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSPISQKIIYKENERFQYKCNMGYEYSERGDAVCTESG----WRPLPSCEEKSCDNPYIP 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GG----PEEATFGNVVRFSCKSRSEILDGSPELYCDERGDWSGPVPKCKAITCAIPPIEN 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSAMEPDREYHFGQAVRFVCNSGYKI-EGDEEMHCSDDGFWSKEKPKCVEISCKSPDVIN 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AEGNDFVFGSKVVYTCQKGYQMVSRINYRRCVAEGWDGVVPVCESQQCPLIHVDNNVQVI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTDGWTNDIPICEVVKCLPVTAPENGKIV 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EASYPGGRQVRVGCNVGYS--GFFKLVCVEGKWETRG--AKCQPRSCGHPGDAQFADFHL 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                      T42921
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                                                                                                                                                                                                                                                                                                                  Fleckenstein, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29.4%; Score 440; DB 2; 36.2%; Pred. No. 8.6e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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                                                                                                                                                                                                                                                     herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108;
                                                                                                                                                                                                                                                        ateles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1053;
      complement factor H repeat hom
                                                                                                                                                                                                                                                     genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6;
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Query Match Best Local Similarity

22.2%;

Score 332.5; DB 2 Pred. No. 3.8e-18;

DB 2;

Conservative

32;

Mismatches

Indels Length

41;

Gaps

8

```
A; Molecule type: mRNA
A; Residues: 80-597 <CH2>
A; Cross-references: GB:X02865; NID:g29564;
A; Note: 92-Thr and 357-His were also found
R; Lintin, S.J.; Reid, K.B.M.
FEBS Lett. 204, 77-81, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: C4BP; proline-rich protein
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Date: 13-Aug-1986 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A33568; S02372; A90326; A24182; A93134; S29492; A31785; I52244; A03210
R;Matsuguchi, T.; Okamura, S.; Aso, T.; Sata, T.; Niho, Y.
Biochem. Biophys. Res. Commun. 165, 138-144, 1989
A;Title: Molecular cloning of the CDNA coding for proline-rich protein (PRP): identity
                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 203-288 <LIN>
A; Residues: 203-288 <LIN>
A; Cross-references: EMBL: X04284; EMBL: X04296
R; Rodriguez de Cordoba, S.; Sanchez-Corral, P.; Rey-Campos, J. Exp. Med. 173, 1073-1082, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Chung, L.P.; Bentley, D.R.; Reid, K.B.M.
Biochem. J. 230, 133-141, 1985
A;Title: Molecular cloning and characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:M31452; NID:g190501; PIDN:AAA36507.1; A;Note: the authors translated the codon GGA for residue 492 R;Lintin, S.J.; Lewin, A.R.; Reid, K.B.M.
                                                                                       A; Contents: annotation; exon-intron boundaries R; Chung, L.P.; Gagnon, J.; Reid, K.B.M. Mol. Immunol. 22, 427-435, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Note: although the sequence determined extends to residue 9 above, R; Chung, L.P.; Bentley, D.R.; Reid, K.B.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
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                              A; Title: Amino acid sequence studies of human C4b-binding protein: N-terminal sequence ced by cyanogen bromide treatment.
                                                                                                                                                                            A; Title: Structure of the gene coding for the alpha A; Reference number: A43023; MUID: 91217619
                                                                                                                                                                                                                                                                                                                                                                                                             A; Title: Studies on the structure of the human A; Reference number: A24182; MUID:86301119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A90326; MUID:86025405
A;Accession: A90326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Derivation of the sequence of the signal peptide A; Reference number: S02372; MUID:88242821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-597 <MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A33568; MUID: 90073699
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                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: A24182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X07853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 17-81 <LI2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 232, 328-332,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: A33568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4b-binding protein alpha chain precursor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGDAVCTESGWRP-LPSCEEKS---CDNPYIPNGD 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KQCSETGRWVPDEETKCEFKVCKIPQVANGHVEVRKT--SNNVQYQYVNIKCDKGFRLQG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWTPRPPICEITKCKPPPTIANGTHTNI-----KEYYTYLDAVTYSCNDETKLTLTGPSS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAYYTCNEGYQLLGEINYREC--DTDG-- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -WINDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYK--IEGDEE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -ECQKRRCSTPADLLNGWYTVT-GNLY-YGSVITYTCNTGYQLLGSPT-SSCLLGPDGRV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PKRNRYVSLRYVNITN--SSGSYPNGTTLQVTCRKGY--IGRQIQTVTCVNGNWTVPN-- 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRRNTEI-----LTGSWSDQTYPEGTQAIYKCRPGYRSLGNVI--MVCRKGEWVALNPL 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1-597 <MA1>
         number: A93134; MUID:8529600J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the
                                                                                                                                                                                                           polypeptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ij
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as Glu
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      밁
                                                      Qy
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                                                                                                                                                                                                                                      Matches
119 -- LRNGQVEIKTDLSFGSQIEFSCSEGFFLIGSTTSR-CEVQDRGVGWSHPLPQCEIVKC
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A:Map position: 1q32-1q32

A:Introns: 48/1; 110/1; 143/2; 172/1; 236/1; 297/1; 362/1; 425/1; 482/1; 540/3

C:Complex: octamer of seven alpha chains and one beta chain
C:Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
C:Keywords: acute phase; chylomicron; complement pathway; duplication; glycoprotein;
F:1-48/Domain: signal sequence #status predicted CSIC>
F:49-597/Product: C4b-binding protein alpha chain #status predicted <MAT>
F:50-108/Domain: complement factor H repeat homology <FH1>
F:50-108/Domain: complement factor H repeat homology <FH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:M62486; NID:g190498; PIDN:AAA36506.1; PID:g190500 C;Comment: C4BP controls the classical pathway of complement activation. It binds as the degradation of the C4bC2a complex (C3 convertase) by dissociating the complement C;Comment: C4BP occurs in plasma in two forms, both of which bind complement fragment isulfide bonds. The beta chain binds the vitamin K-dependent plasma protein S. A mino actors V and VIII.
                                                                                                                               F;113-170/Domain: complement factor H repeat homology <FH2>F;175-234/Domain: complement factor H repeat homology <FH3>F;239-294/Domain: complement factor H repeat homology <FFH4>F;239-360/Domain: complement factor H repeat homology <FH5>F;364-422/Domain: complement factor H repeat homology <FH6>F;381-404/Region: complement C4b binding #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Aso, T.; Okamura, S.; Matsuguchi, T.; Sākamoto, N.; Sata, T.; Niho, Y. Biochem. Biophys. Res. Commun. 174, 222-227, 1991
A;Title: Genomic organization of the alpha chain of the human C4b-binding A;Reference number: I52244; MUID:91113199
A;Accession: I52244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: protein
A:Residues: 495-505, 'X', 507-510, 'X', 512-515 <SUZ>
A:Residues: 495-505, 'X', 507-510, 'X', 512-515 <SUZ>
A:Note: this peptide appears to bind protein S
R:Dahlback, B.; Smith, C.A.; Muller-Eberhard, H.J.
Proc. Natl. Acad. Sci. U.S.A. 80, 3461-3465, 1983
A:Title: Visualization of human C4b-binding protein and its complexes with vitamin K-A;Reference number: A93950; MUID:83221615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Note: this paper reports amino-terminal sequences of the intact protein and of a nu R;Hessing, M.; Kanters, D.; Takeya, H.; van't Veer, C.; Hackeng, T.M.; Iwanaga, S.; B FEBS Lett. 317, 228-232, 1993
A;Title: The region Ser(333)-Arg(356) of the alpha-chain of human C4b-binding protein A;Reference number: S29492; MUID:93146164
A;Accession: S29492
                                             F;426-480/Domain: complement factor H repeat homology <FH7>F;484-538/Domain: complement factor H repeat homology <FH8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Comment: The molecule has a central body supporting seven tentacles (alpha chains).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-597 <ASO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Reference number: A31785; MUID:89034204 A;Accession: A31785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biol. Chem. 263, 17034-17039, 1988
A;Title: Binding site for vitamin K-dependent protein S on complement C4b-binding pro
F;221,506,528/Binding site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GDB:120568; OMIM:120830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB:C4BPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: translation not shown; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 381-404 <HES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: A93134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 annotation; electron microscopy; three-dimensional structure; ligand bind
carbohydrate (Asn) (covalent) #status
     experimental
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20 SDQTYPEGTQAIYKCRPGY-RSLGNVIMVCRK-GEWVALNPLRKCQKRPCGHPGDTPFGT 77

FTLTGGNV-----FEYGVKAVYTCNEGYQLLGEINYRECDTD----GWTNDIPICEVVKC 128

TETRFKTGTTLKYTCLPGYVRSHSTQTLTCNSDGEWV-YNTF--CIYKRCRHPGE----- 118

Local

Similarity

20.2%;

Score 303; DB 1; Pred. No. 1.1e-15; Mismatches 101;

Indels

Gaps

16;

Conservative

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A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1989 #sequence_revision 30-Jun-1990 #text_change 22-Jun-1999
_C;Accession: A31005; B42504
                                                                                                                                                         apolipoprotein H homolog precursor - vaccinia virus N;Alternate names: 35K secretory protein; C3L prote C;Species: vaccinia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;112-169/Domain: complement factor H repeat homology <FH2>F;174-234/Domain: complement factor H repeat homology <FH3>F;239-294/Domain: complement factor H repeat homology <FH4>F;239-294/Domain: complement factor H repeat homology <FH4>F;299-360/Domain: complement factor H repeat homology <FH5>F;364-422/Domain: complement factor H repeat homology <FH7>F;364-482/Domain: complement factor H repeat homology <FH7>F;486-480/Domain: complement factor H repeat homology <FH8>F;484-538/Domain: complement factor H re
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C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
F;50-107/Domain: complement factor H repeat homology <FH1>
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A; Residues: 1-597 < DEF>
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A; Accession: S53711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 WSDPLPKCEIVKCEPPPNIINGKHNGG----NEDIHTYGSSVTYSCNPRFSLLGEASISC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 KPPPDIRNGRHSGE----ENFYAYGFSVTYSCDPRFSLLGHASISCTVENETIGVWRPSP 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 LPVTAPENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDD-----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              276 SSLIHCELDSKWNPSPPVCESNSCLGLPNVPH 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          230 DAV--C-TESGWRPLPS-CEEKSC-DNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218 TVKNKTVGVWSPSPPVCKEIICSPPNVPHGKIISGFGPIYNYKDSIMYTCIDGFVL--RG 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                105 TFCVKKRCRNPGDLPNGQVEVK--TDFSFGSQIEFSCSEGYILIGSTT-SHCDIQEKGVE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 SPPACEPNSCINLPDIPHASW 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         241 L-PSCEEKSCDN-PYIPNGDY 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 RKCQKRPCGHPGDTPFGTFTLTGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTD----G 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S----DDGFWSKEKPKCVEISCKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTNDIPICEVVKCLPVTAPENGKIVSSAMEPDREYH-FGQAVRFVCNSGYKIEGDEEMHC 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTCEKITCRKPDVSHGEMVSGFGPIYNYKDTIVFKCQKGFVL--RGSSVIHCDADSKWNP 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DCGP-PPHLLFASSISELSENEYQTGTILKYTCRPGYTRNGLNPILTCKPRGLW---SYD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                 protein; virokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 597;
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complement C3b receptor type 2 long form precursor - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C;Accession: A45900; 143306
R;Kurtz, C.B.; O'Toole, E.; Christensen, S.M.; Weis, J.H.
J. Immunol. 144, 3581-3591, 1990
A;Title: The murine complement receptor gene family. IV. Alternative splicing
A;Reference number: A45900; MUID:90229754
A;Accession: A45900
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A;Title: Appendix to The complete DNA sequence of vaccinia virus"
A;Cross-references: GB:M36470
A;Experimental source: clone 31-1
R;Kim, Y.U; Kinoshita, T.; Molina,
J. Exp. Med. 181, 151-159, 1995
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A;Title: The complete DNA sequence of vaccinia virus.
A;Reference number: A42531; MUID:91021027
                                                                                                                                                              A; Residues: 1-676 < KUR>
                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A45900
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F;206-261/Domain: complement factor H repeat homology <FH4>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Note: neither amino acid nor nucleotide sequence is given C; Superfamily: herpesvirus complement control protein; comp
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A;Experimental source: strain WR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Title: Vaccinia virus encodes a secretory polypeptide structurally related to compl A; Reference number: \tt A31005;\ MUID:88318974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Kotwal, G.J.; Moss, B. Nature 335, 176-178, 1988
                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M35027; NID:g335317; PIDN:AAA47997.1; PID:g335345
A;Experimental source: strain Copenhagen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: B42504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A42501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-263 <KOT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: A31005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 HPTISNGYLSSGFKRSYSYNDNVDFKCKYGYKLSGSSSSTCSPGNTWKPELPKC 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194 SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               154 ISNGR--HNGYED--FYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-DPPTCQIVKCP 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97 LDIGG----VDFGSSITYSCNSGYHLIGESKSYCELGSTGSMVWNPEAPICESVKCQSPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 20.1%; Score 301.5; DB 1; Length 263; Local Similarity 33.3%; Pred. No. 6.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFN---QCIKRRCPSPRDIDNGQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-263 <GOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G.P.; Perkus, M.E.; Davis, S.W.; Winslow, J.P.; Paoletti, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Mismatches
                                            H.; Hourcade, D.; Seya, T.; Wagner, L.M.; Holers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement factor H repeat hom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type; DNA
A;Residues: 1-683,'X',685-1133,'X',1135-1471,'X',1473-2489
                                                                                                                                                                                                                                                                 J. Immunol. 151, 6214-6224, 1993
A; Title: Structure of the gene f
                                                                                                                                                                                                                                                                                                R; Vik, D.P., Wong,
J. Immunol. 151, 62
                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 24-Nov-1999 #text_change 31-Jan-2000
C;Accession: 173012; 156203; A47602; S03291; S03843; A28507; A24748; B24748
                                                                                                                                                                                                                                                                                                                                                                                                                     complement C3b/C4b receptor, membrane-bound form precursor - human N;Alternate names: complement C3b/C4b receptor; complement receptor type 1 (CR1); surface N;Contains: complement C3b/C4b receptor, secreted form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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                                                                                                       A;Cross-references: GB:L17418; NID:g306678; PID:g451303
                                                                                                                                                                                                                    A; Accession: 173012
                                                                                                                                                                                                                                             A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;145-211/Domain:
F;217-272/Domain:
F;276-331/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;22-78/Domain: complement factor H repeat homology  F;83-140/Domain: complement factor H repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Introns: 80/1; C; Superfamily: c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: Cr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U17128; NID:g595980; PIDN:AAA78271.1; PID:g595982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Mouse complement regulatory protein Crry/p65 uses the specific mechanisms of bd
A;Reference number: I48306; MUID:95105691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;467-523/Domain:
F;531-587/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;399-458/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;336-394/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 21-367 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A; Accession: I48306
                           Molecule type: DNA
                                                     Status: translated from GB/EMBL/DDBJ
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 PSCEEKSCDNPYIPN 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           269 LPTCFMGCLPPQNILHGDYNKKDEFFSVGQKVSYTCNPGYTLIGTNLVECTSLGTWSNTV 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             185 PKCV-EISCKSPDVING-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95 HINTG--IEFGSTITYSCNQGYRLIGD-SSATCIVSDNTVMWDNDMPLCESIPCESPPAI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 TLTGGNVFEYGVKAVYTCNEGYQLLGEINYREC----DTDGWTNDIPICEVVKCLPVTAP 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDQT-YPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTF 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SNGDFYSSSRD----SFFYGMVVTYYCHTGKNREKLFDLVGEKSIYCTSKDNQVGIWNSPP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGKIVSSAMEPDREYHFGQAVRFVCNSG-----YKIEGDEEMHCSDD-----GFWSKEK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDKSEFAIGTTWEYKCRPGYFRKSFIITCLETSKW--SDAQQFCKRKPCMNPQEPLHGSV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQCIPRVKCPMPEIENGLVESGFKHSFFLNDTVIFKCKSGFTMKGSRIAWCQPNSKWSPP 268
1-683,'X',685-894,'A',896-1000,1451-1471,'X',1473-2489 <VIK2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement factor H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement factor H repeat homology <FH03>
complement factor H repeat homology <FH04>
complement factor H repeat homology <FH05>
complement factor H repeat homology <FH05>
complement factor H repeat homology <FH07>
complement factor H repeat homology <FH07>
complement factor H repeat homology <FH09>
complement factor H repeat homology <FH009>
complement factor H repeat homology <FH109>
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                                                                                                                                                                                                                                                                                                                              Ψ.
Ψ.
                                                                                                                                                                                                                                          of the gene for the F allele of complement receptor type 1 and sequent 156203; MUID:94065175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20.1%; 26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 301; DB 2; Length 676; Pred. No. 1.8e-15; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             repeat homology
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                                                                                                                                                                                                                                                                                                                                               A24748; B24748; C24748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16;
                                                                        F;943-999/Domain: complement
                                                                                                                           F;808-866/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB:CR1; CD35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 26-584 <H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S03291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: A47602
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                                                                                                                           complement
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F:42-584/Product: complement C3b/C4b receptor, secreted form #status predicted <MATS>
F:43-99/Domain: complement factor H repeat homology <FH01>
F:104-161/Domain: complement factor H repeat homology <FH02>
F:166-232/Domain: complement factor H repeat homology <FH03>
F:238-293/Domain: complement factor H repeat homology <FH04>
                                                                                  F;1004-1061/Domain: complement factor
                                                                                                                                                                                                                                                       F:554-611/Domain: complement factor H repeat
F:616-682/Domain: complement factor H repeat
F:688-743/Domain: complement factor H repeat
F:7447-803/Domain: complement factor H repeat
                                                                                                                                                                                                                                                                                                                                         F;238-293/Domain: complement factor H repeat homology <FH004>
F;297-353/Domain: complement factor H repeat homology <FH054>
F;358-416/Domain: complement factor H repeat homology <FH065>
F;358-416/Domain: complement factor H repeat homology <FH075>
F;421-487/Domain: complement factor H repeat homology <FH075>
F;493-549/Domain: complement factor H repeat homology <FH095>
F;451-682/Domain: complement factor H repeat homology <FH095>
F;616-682/Domain: complement factor H repeat homology <FH105>
F;616-682/Domain: complement factor H repeat homology <FH105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            F:42-2489/Product: complement C3b/C4b receptor, membrane-bound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: C4b-binding protein alpha chain; complement factor C;Keywords: duplication; glycoprotein; transmembrane protein F;1-41/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Map position: 1q32-1q32
A; Introns: 41/1; 101/1; 134/2; 163/1; 296,
; 1494/2; 1513/1; 1646/1; 1705/1; 1739/2;
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R;Klickstein, L.B.; Bartow, T.J.; Miletic, V.; Rabson, L.D.; Smith, J.A.; Fearon, D.T.
J. Exp. Med. 168, 1699-1717, 1988
A;Title: Identification of distinct C3b and C4b recognition sites in the human C3b/C4
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R;Wong, W.W.; Cahill, J.M.; Rosen, M.D.; Kennedy, C.A.; Bonaccio, E.T.; Morris, M.J.;
J. Exp. Med. 169, 847-863, 1989
A;Title: Structure of the human CR1 gene. Molecular basis of the structural and quant
A;Reference number: A47602; MUID:89176869
                                                  F;1066-1132/Domain: complement
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A; Residues: 311-333;729-745;831-845 <WO2>
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A;Accession: A24748
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A; Residues: 953-1221, FV', 1224-2064, 'I', 2066-2276, 'p', 2278-2299, 'H', 2301-2325, 'T', 232
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A;Accession: S03843
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A;Cross-references: EMBL:X14362; NID:930197; PID:9736240
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1; 1705/1; 1739/2; 1768/1; 1844/1; 1904/1; 1937/2; 1966/1; 209
ing protein alpha chain; complement factor H repeat homology
                                                                                                                           factor H repeat homology <FH14>
                                                                                                                                                                                                                       factor H repeat homology <FH13>
                                         factor
H repeat
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                                                                                                                                                                                                                                                  nomology <FH11>
homology <FH12>
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F:1258-1316/Domain:
F:1321-1387/Domain:
F:1393-1449/Domain:
F:1393-1449/Domain:
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F:1516-1582/Domain:
F:1588-1643/Domain:
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F:1907-1837/Domain:
F:1907-1964/Domain:
F:1907-1964/Domain:
F:1907-2035/Domain:
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F:2041-2096/Domain:
F:2041-2096/Domain:
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change 31-Jan-2000
C;Date: 02-Jul-1996 *sequence_revision 02-Jul-1996 *text_change 31-Jan-2000
C;Accession: 136936; 136937
R;Birmingham, D.J.; Shen, X.P.; Hourcade, D.; Nickells, M.W.; Atkinson, J.P.
J.Immunol. 153, 691-700, 1994
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A;Gene: CR1
C;Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology
                                                   A;Cross-references: GB:L24921; NID:g557726; PID:g557727 C;Genetics:
                                                                                        A; Molecule type: mRNA
A; Residues: 1-397,1751-2014 <BIR2>
                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-2014 <BIR1>
                                                                                                                                                                                                                               A;Title: Primary sequence of an alternatively spliced form of CR1. Candidate for the 75 A;Reference number: 136935; MUID:94292799 A;Accession: 136936
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2359-2415/Domain:
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F:470-526/Domain: complement factor H repeat homology <FH08>
F:529-586/Domain: complement factor H repeat homology <FH09>
F:722-778/Domain: complement factor H repeat homology <FH10>
F:172-178/Domain: complement factor H repeat homology <FH10>
F:172-1228/Domain: complement factor H repeat homology <FH11>
F:1172-1228/Domain: complement factor H repeat homology <FH12>
F:1233-1291/Domain: complement factor H repeat homology <FH13>
F:1296-1362/Domain: complement factor H repeat homology <FH15>
F:1432-1489/Domain: complement factor H repeat homology <FH15>
F:165-1681/Domain: complement factor H repeat homology <FH15>
F:165-1681/Domain: complement factor H repeat homology <FH15>
F:165-1681/Domain: complement factor H repeat homology <FH16>
F:165-1681/Domain: complement factor H repeat homology <FH16>
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A; Molecule type: protein
A; Residues: 39-51 <SA2>
A; Residues: 39-51 <SA2>
C; Comment: This protein plays a critical role in protection against complement mediat C; Superfamily: C4b-binding protein alpha chain; complement factor H repeat homology C; Keywords: glycoprotein; transmembrane protein
F; 1-36/Domain: signal sequence *status predicted <SIG>
F; 37-488/Product: complement regulatory protein, 512 antigen *status predicted <MAT>
F; 38-94/Domain: complement factor H repeat homology <FH1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement regulatory protein, 5I2 antigen precursor - rat C;Species: Rattus norvegicus (Norway rat) C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_clC;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_clC;Accession: JC2054; PC2027
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A;Title: Molecular cloning of the rat complement regulatory protein, 512 antigen.
A;Reference number: JC2054; MUID:94161746
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A; Residues: 1-497 <SA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -RCRRKSCRNPPDPVNGMVHVI--KDIQFGSQIKYSCTKGYRLIGS-SSATCIISGDTVI 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---IPNGDYSP 261
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26.6%;
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homology <FH17>
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A;Residues: 1-263 <BLI>
A;Cross references: GB:X69198; NID:g456758; PIDN:CAA48953.1; PID:g297195 C;Superfamily: herpesvirus complement control protein; complement factor H repeat homology <FH2> F;21-81/Domain: complement factor H repeat homology <FH2> F;86-143/Domain: complement factor H repeat homology <FH3> F;148-201/Domain: complement factor H repeat homology <FH4> F;148-201/Domain: complement factor H repeat homology <FH4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N;Alternate names: D12L protein
C;Species: variola virus
C;Date: 10-Sep-1999 #sequence_revision
C;Accession: C36838
R;Blinov, V.M.
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F:161-227/Domain: complement factor H repeat homology <FH3>
F:233-288/Domain: complement factor H repeat homology <FH4>
F:233-294-352/Domain: complement factor H repeat homology <FH5>
F:357-413/Domain: complement factor H repeat homology <FH6>
F:357-413/Domain: complement factor H repeat homology <FH6>
F:421-444/Domain: transmembrane #status predicted <TMM>
F:421-444/Domain: transmembrane #status predicted <TMM>
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A; Accession: C36838
A; Molecule type: DNA
A; Residues: 1-263 <BLI>
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Best Local :
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Best Local :
194 SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                   154
                                                                                          134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 PSC-EEKSCDN--PYIPNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 QCIELNKCTPPHVENAVIVSKNKSLFSLRDMVEFRCQDGFMMKGDSSVYCRSLNRWEPQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 --NTDIRFGSSITYTCNEGYRLIGSSSAMCIISDQSVAWDAEAPICESIPCEIPPSIP-N 169
                                                                                                                                                97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21 DQTYPEGTQAIYKCRPGYRSLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGTFTL 80
                                                                                                                                                                                          78
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                                              ISNGRHNGY----NDFYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-NPPTCQIVKCP
                                                                                                                                                                                     FTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---WTNDIPICEVVKCLPVTA 133
                                                                                                                                                                                                                                      ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFN---QCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                SDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCVEIS-CKSPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTE-SGWRP-L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDFFS----PNREDFHYGMVVTYQCNTDARGKKLFNLVGEPSIHCTSIDGQVGVWSGPPP
                                                                                                                                         LDIGG----VDFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GKIVSSAMEPDRE-YHFGQAVRFVCNSG-----YKIEGDEEMHCS----DDGFWSKEKP 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGNVFEYGVKAVYTCNEGYQLLGEINYRECDTD---GWTNDIPICEVVKC-LPVTAPEN 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESTFPVGTSLKYECRPGYIKRQFSITCEVNSVWT--SPQDVCIRKQCETPLDPQNGIVHV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18; Conserv
                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A36859
                                                                                                                                                                                                                                                                                                                                                         19.0%;
32.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19.3%;
30.1%;
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                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                 Score 284.5; DB 1
Pred. No. 1.2e-14;
9; Mismatches 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 289.5; DB 2; Pred. No. 9.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108;
                                                                                                                                                                                                                                                                                                                                                                             Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement factor H repeat homol
                                                                                                                                                                                                                                                                                                                                 Indels
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R:Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox vir A;Reference number: Z20488; MUID:94088747
A;Accession: T28450
                                                                                                                                                      Qγ
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                                                                                                                                                                                                                                                                                      Вр
                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:L22579; PIDN:AAA60760.1
A;Experimental source: strain "Bangladesh-1975"
C;Superfamily: herpesvirus complement control pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T28450
hypothetical protein D15L - variola major virus
C:Species: variola major virus
Search completed:
Job time: 366 sec
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A; Residues: 1-263 <MAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 11-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                      194
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                                                                                                                                                                                                                                      134 PENGKIVSSAMEPDREYHFGQAVRFVCNSGYKIEGDEEMHCSDDGFWSKEKPKCVEISCK 193
                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                             78 FTLTGGNVFEYGVKAVYTCNEGYQLLGEI-NYRECDTDG---WTNDIPICEVVKCLPVTA 133
                                                                                                           HPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC
                                                                                                                                                  SPDVINGSPISQ-KIIYKENERFQYKCNMGYEYSERGDAVCTESG-WRP-LPSC 244
                                                                                                                                                                                             ISNGRHNGY----NDFYTDGSVVTYSCNSGYSLIGNSGVLCS-GGEWS-NPPTCQIVKCP
                                                                                                                                                                                                                                                                                  LDIGG----VDFGSSITYSCNSGYYLIGEYKSYCKLGSTGSMVWNPKAPICESVKCQLPPS 153
                                                                                                                                                                                                                                                                                                                                                                         ANANYNIGDTIEYLCLPGYRKQKMGPIYAKCTGTGWTLFN---QCIKRRCPSPRDIDNGH 96
                                                                                                                                                                                                                                                                                                                                                                                                                    SDQTYPEGTQAIYKCRPGYR--SLGNVIMVCRKGEWVALNPLRKCQKRPCGHPGDTPFGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPTILNGYLSSGFKRSYSYNDNVDFTCKYGYKLSGSSSSTCSPGNTWQPELPKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
75; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T28450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                      November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.0%;
                    21,
                      2000, 16:47:37
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 284.5; DB 2
Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       control protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                109;
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